

SEQUENCE LISTING

<110> Patience, Clive

<120> Gamma Herpes Virus DNA and Methods of Use

<130> 61750-379

<150> US/09/612,204

<151> 2000-07-07

<150> US/60/142,736

<151> 1999-07-08

<150> US/60/168,532

<151> 1999-12-02

<160> 55

<170> PatentIn version 3.0

<210> 1

<211> 585

<212> DNA

<213> artificial

<220>

<223> Fragment from Swine Gamma Herpesvirus DNA coding for glycoprotein B envelope protein

<400> 1

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cagcatagag ctgctctgg	gtggaatgag	ctcagcaaga	ttaatccac	120
agcatgattt acaatagacc	cgtatcagcc	aaaagaata	gagatgtcat	180
aaactgtattt	tggttagacca	aaccagtgtc	tcattacata	240
gcacatcgat	aaaagtgc	ctctagac	aaagtctcag	300
actatttaca	aaggcaact	aggagtcaat	aatgagattc	360
gaaacatgtc	aggaaaacac	tgagtattac	tcttaaccac	420
aaaaactatg	agcatttgaa	gactgtgc	ttatctcga	480
atagccctta	atttacact	tttgacttta	tcaccacact	540
agggacgaga	agaggcttag	taatgtctt	agatacatt	585

<210> 2

<211> 195

<212> PRT

<213> artificial

<220>

<223> Deduced amino acid sequence derived from the first open reading frame of the DNA of SEQ ID NO:

<400> 2

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Trp Cys Arg Glu Gln His Arg Ala Ala Leu Val Trp Asn Glu Leu Ser

20	25	30
Lys Ile Asn Pro Thr Ser Val Met Ser Met Ile Tyr Asn Arg Pro Val		
35	40	45
Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser Asn Cys Ile Val		
50	55	60
Val Asp Gln Thr Ser Val Ser Leu His Lys Ser Leu Arg Leu Leu Ser		
65	70	75
Ala Ser Asp Glu Lys Cys Phe Ser Arg Pro Pro Val Thr Phe Lys Phe		
85	90	95
Met Asn Asp Ser Thr Ile Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu		
100	105	110
Ile Leu Leu Thr Thr Tyr Leu Glu Thr Cys Gln Glu Asn Thr Glu		
115	120	125
Tyr Tyr Phe Gln Ala Lys Thr Asp Met Tyr Ile Tyr Lys Asn Tyr Glu		
130	135	140
His Leu Lys Thr Val Pro Leu Ser Ser Ile Thr Thr Leu Asp Thr Phe		
145	150	155
Ile Ala Leu Asn Phe Thr Leu Leu Glu Asn Val Asp Phe Lys Val Ile		
165	170	175
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180	185	190
Glu Thr Met		
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<211> 19		
<212> DNA		
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<223> PCR amplification primer for pGHV-gpB gene sequences		
<400> 3		
mgaacaacgt yaaytgyga		19
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<400> 4		
mgaacaacgt yaaytgyct		19

<210> 5  
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cartcartwt gcmtaygac

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<210> 7  
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<221> misc\_feature  
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carntncart wtgcmtayg

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gtbatgwsha gvathtaygg

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<210> 9  
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swcatnacrs tngtnggrtt

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<210> 11  
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<220>  
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gtartarttr taytcyctra a

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<400> 13  
ctgraartt r taytcycgra a

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<223> PCR amplification primer for Epstein-Barr Virus genome

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agaactaccg tcaactgcct

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<210> 16  
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<223> PCR amplification primer for Epstein-Barr Virus genome

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<220>  
<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 17  
cagatccaat ttgcctacga c

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<400> 18  
cagatccaaat ttgcctacg 19

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<400> 20  
gacatgacgg tggttggatt 20

<210> 21  
<211> 26  
<212> DNA  
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<220>  
<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 21  
tgcgcctgga agttgtactc ccggaa 26

<210> 22  
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<212> DNA  
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<220>  
<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 22

ctggaagttg tactcccgga a

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<210> 23

<211> 2598

<212> DNA

<213> artificial

<220>

<223> cDNA for porcine gamma herpesvirus gpB gene

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tggctactg aatcgccgct aacaggtcac tatggAACAC acgattcaag ccatggtaaa	180
agaggAAAACA acgAAAACAG agattcAGAA gagCAAATA aaaacATTAA tggatcgccc	240
tctacgtttc cttacagagt atgcAGTGCc tccggAGTTG gagATGTCTT tagatttcAG	300
accgaccatg tggTCCCGA tgccAGTGTat atggTacaCA gtgaggGGAT tctactaATT	360
tacAAACAGA acattattCC atttatGTT agagTTAGGA aatataGAAA agttgttACA	420
acaAGTACTG tctacaATGG tatttattCT gactCTATTA ccaACCAACA tactttCTAT	480
aaatcaATCG aacCTTGGGA gacAGAAAAG atggacACAA tatATCAGTG ttttAAATTCT	540
ttaAGACTAA acacAGGTGG aaATCTGCTT acttATGTag atAGAGATGA tataAAATATG	600
acAGTGTTC tgcaACCTGT tgacGGTGTG acgCCCAGTG tgaAGAGGTA tggcAGTCAA	660
ccAGAGCTGT acCTTGAAcc tggCTGGTT tggggTAGTT atagaAGACG aactACAGTG	720
aactGTGAAC taatGGACAT gtttGCAAGA tcaaATCCTC cattGATTt ctttGTTACA	780
gctacAGGTG atacGGTGGA aatGTCCTCA ttttGGAGTG gtGAAGATGA tcatGAAAAT	840
aagatGcAcG agaAGCCATG gtttGTTAGT gtGATAAATA actACAAAGGT ggtGGACTAT	900
caAAACAGAG ggACTGTACC CCTTGGAAAAA acaAGGATAT ttCTAGATAG ggaAGAGTAT	960
acattatCTT gggAAAAGCA tctaAAAAT atGTCATATT gtcCActAAcC attatGGAAA	1020
gcattttACA atGGAATCCA gacGGAGCAT tcaggCTCAT atcattttGT agccaATGAC	1080
atCACAGCGT cattcacaAC tagtAAAGAA gacATGAAAG agttCAATAC gacATATCAT	1140
tgtctcaACG aggAAATAAA ggcAGAAATA gagaAGAAAT atGCAAAGT aaACTCAACT	1200
cactCTAAAT atGGAGATCT gaaATACTT AAAACAGATG gggGTCTCTA tttagtCTGG	1260
caacCTCTTA ttcaAAACAG gcttCTTGTat gctaAGAAcA aactGAACAA tgAGACTTAT	1320
tccaggAGAT cacGACGTCA ggcAGAAATCT actACTGACC caatGATGGA gatGACTGGA	1380
aatGGAGCAG gtggAGAAATA tagcAGTGAa aattcaATCA cggtGGCGCA ggtGcAGTAT	1440
gcctatGACA atCTTCGTat cagaATAAAT aacattttGG aagatttGTC aaaggcatGG	1500
tgtcGTGAGC agcatAGAGC tgctCTGGTG tggAAATGAGC tcAGCAAGAT taatCCACa	1560
agcGTcatGA gcatGATTa caatAGACCC gtatCAGCA aAAGAATAGG agatGTCATT	1620
tcAGTCTCTA actGTATTGT ggtAGACCAA accAGTGTCT cattACATAA aagtCTCAGG	1680
cttCTCAGTG catCGGATGA aaAGTGTCTC tctAGACCTC cAGTGAcATT taagTTATG	1740
aatGACAGTA ctatttACAA aggGCAACTA ggAGTCAATA atGAGATTCT ttAAACCACa	1800
acataCCTG aaACATGTCA ggAAAACACT gAGTATTACT ttCAGGCAAA gACAGACATG	1860
tacatttACA AAAACTATGA gcatttGAAG actGTGcCTT tatCTCgAT caccACACTA	1920
gatacattTA tagCCCTTA ttTACACTA ttggAGAAATG ttGACTTTAA agtCATTGAA	1980
ctttataCCA gggACGAGAA gagGCTTAGT aatGTCCTTG acattGAAAC aatGTTTAgG	2040
gaatataACT actATGCTCA gagGGTcAGT ggcCTCAGAA aggATTGcT gGATCTAAGC	2100
accaATAGAA atCAATTGTG gGATGcATTt ggtAGTCTTA tggATGATTt gggTGTGTT	2160
gggcAGAGAG ttGTAATGc tgtaAGTGGT gtggCTACGc tgTTAGCTC aattGTAACA	2220
ggatttATAA atttCATTAA aaACCCATTt ggtGGAATGT taatGATTAT tggTTATT	2280
ggTGTGCTAT ttGCCATCTA ctTTCTGACC AAAAAGACGA agatATATGA gacGGCACCG	2340
attaAGATGA ttTATCCTGA aattGACAAG ctGAAAGAAC gtGAGGGAAA atcAGAAATA	2400
gcaccaATCA gtGAAGAAGA gctGGAGAGA attGTACTTG ctATGcACAT ccatCAACAA	2460
aattcACATA tggAAACAAA aacaAGGAAG gatCCCAAG acAGCATATT aacaAGGGCA	2520
caAAATATGC tacGCAAAG atCAGGATAT tctaATTAA AAAATGCTGA atCTGTGGAG	2580
atGTTAAACA otTTATAA	2598

<210> 24  
<211> 865  
<212> PRT  
<213> artificial

<220>

<223> Deduced amino acid sequence of porcine gamma herpesvirus gpB gene

<400> 24

Met Ala Gly Ser Leu Lys Leu Arg Gly Ser Val Leu Ala Leu Trp Tyr  
1 5 10 15

Leu Tyr Gln Val Ala Leu Tyr Ser Leu Ser Ile Ala Glu Thr Gly Val  
20 25 30

Thr Ser Pro Pro Asn Thr Ala Thr Trp Ser Thr Glu Ser Pro Leu Thr  
35 40 45

Gly His Tyr Gly Thr His Asp Ser Ser His Gly Glu Arg Gly Asn Asn  
50 55 60

Glu Asn Arg Asp Ser Glu Glu Gln Asn Lys Asn Ile Tyr Gly Ser Pro  
65 70 75 80

Ser Thr Phe Pro Tyr Arg Val Cys Ser Ala Ser Gly Val Gly Asp Val  
85 90 95

Phe Arg Phe Gln Thr Asp His Val Cys Pro Asp Ala Ser Asp Met Val  
100 105 110

His Ser Glu Gly Ile Leu Leu Ile Tyr Lys Gln Asn Ile Ile Pro Phe  
115 120 125

Met Phe Arg Val Arg Lys Tyr Arg Lys Val Val Thr Thr Ser Thr Val  
130 135 140

Tyr Asn Gly Ile Tyr Ser Asp Ser Ile Thr Asn Gln His Thr Phe Tyr  
145 150 155 160

Lys Ser Ile Glu Pro Trp Glu Thr Glu Lys Met Asp Thr Ile Tyr Gln  
165 170 175

Cys Phe Asn Ser Leu Arg Leu Asn Thr Gly Gly Asn Leu Leu Thr Tyr  
180 185 190

Val Asp Arg Asp Asp Ile Asn Met Thr Val Phe Leu Gln Pro Val Asp  
195 200 205

Gly Val Thr Pro Asp Val Lys Arg Tyr Gly Ser Gln Pro Glu Leu Tyr  
210 215 220

Leu Glu Pro Gly Trp Phe Trp Gly Ser Tyr Arg Arg Arg Thr Thr Val  
225 230 235 240

Asn Cys Glu Leu Met Asp Met Phe Ala Arg Ser Asn Pro Pro Phe Asp  
245 250 255

Phe	Phe	Val	Thr	Ala	Thr	Gly	Asp	Thr	Val	Glu	Met	Ser	Pro	Phe	Trp
260															270
Ser	Gly	Glu	Asp	Asp	His	Glu	Asn	Lys	Met	His	Glu	Lys	Pro	Trp	Phe
275															285
Val	Ser	Val	Ile	Asn	Asn	Tyr	Lys	Val	Val	Asp	Tyr	Gln	Asn	Arg	Gly
290															300
Thr	Val	Pro	Leu	Gly	Lys	Thr	Arg	Ile	Phe	Leu	Asp	Arg	Glu	Glu	Tyr
305															320
Thr	Leu	Ser	Trp	Glu	Lys	His	Leu	Lys	Asn	Met	Ser	Tyr	Cys	Pro	Leu
	325														335
Thr	Leu	Trp	Lys	Ala	Phe	Tyr	Asn	Gly	Ile	Gln	Thr	Glu	His	Ser	Gly
	340														350
Ser	Tyr	His	Phe	Val	Ala	Asn	Asp	Ile	Thr	Ala	Ser	Phe	Thr	Thr	Ser
	355														365
Lys	Glu	Asp	Met	Lys	Glu	Phe	Asn	Thr	Thr	Tyr	His	Cys	Leu	Asn	Glu
	370														380
Glu	Ile	Lys	Ala	Glu	Ile	Glu	Lys	Lys	Tyr	Ala	Lys	Val	Asn	Ser	Thr
385															400
His	Ser	Lys	Tyr	Gly	Asp	Leu	Lys	Tyr	Phe	Lys	Thr	Asp	Gly	Gly	Leu
	405														415
Tyr	Leu	Val	Trp	Gln	Pro	Leu	Ile	Gln	Asn	Arg	Leu	Leu	Asp	Ala	Lys
	420														430
Asn	Lys	Leu	Asn	Asn	Glu	Thr	Tyr	Ser	Arg	Arg	Ser	Arg	Arg	Gln	Ala
	435														445
Glu	Ser	Thr	Thr	Asp	Pro	Met	Met	Glu	Met	Thr	Gly	Asn	Gly	Ala	Gly
	450														460
Gly	Glu	Tyr	Ser	Ser	Glu	Asn	Ser	Ile	Thr	Val	Ala	Gln	Val	Gln	Tyr
465															480
Ala	Tyr	Asp	Asn	Leu	Arg	Ile	Arg	Ile	Asn	Asn	Ile	Leu	Glu	Asp	Leu
	485														495
Ser	Lys	Ala	Trp	Cys	Arg	Glu	Gln	His	Arg	Ala	Ala	Leu	Val	Trp	Asn
	500														510
Glu	Leu	Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Ser	Met	Ile	Tyr	Asn
	515														525
Arg	Pro	Val	Ser	Ala	Lys	Arg	Ile	Gly	Asp	Val	Ile	Ser	Val	Ser	Asn
	530														540
Cys	Ile	Val	Val	Asp	Gln	Thr	Ser	Val	Ser	Leu	His	Lys	Ser	Leu	Arg
	545														560

Leu Leu Ser Ala Ser Asp Glu Lys Cys Phe Ser Arg Pro Pro Val Thr  
565 570 575

Phe Lys Phe Met Asn Asp Ser Thr Ile Tyr Lys Gly Gln Leu Gly Val  
580 585 590

Asn Asn Glu Ile Leu Leu Thr Thr Tyr Leu Glu Thr Cys Gln Glu  
595 600 605

Asn Thr Glu Tyr Tyr Phe Gln Ala Lys Thr Asp Met Tyr Ile Tyr Lys  
610 615 620

Asn Tyr Glu His Leu Lys Thr Val Pro Leu Ser Ser Ile Thr Thr Leu  
625 630 635 640

Asp Thr Phe Ile Ala Leu Asn Phe Thr Leu Leu Glu Asn Val Asp Phe  
645 650 655

Lys Val Ile Glu Leu Tyr Thr Arg Asp Glu Lys Arg Leu Ser Asn Val  
660 665 670

Phe Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Arg  
675 680 685

Val Ser Gly Leu Arg Lys Asp Leu Leu Asp Leu Ser Thr Asn Arg Asn  
690 695 700

Gln Phe Val Asp Ala Phe Gly Ser Leu Met Asp Asp Leu Gly Ala Val  
705 710 715 720

Gly Gln Thr Val Val Asn Ala Val Ser Gly Val Ala Thr Leu Phe Ser  
725 730 735

Ser Ile Val Thr Gly Phe Ile Asn Phe Ile Lys Asn Pro Phe Gly Gly  
740 745 750

Met Leu Met Ile Ile Val Val Ile Gly Val Leu Phe Ala Ile Tyr Phe  
755 760 765

Leu Thr Lys Lys Thr Lys Ile Tyr Glu Thr Ala Pro Ile Lys Met Ile  
770 775 780

Tyr Pro Glu Ile Asp Lys Leu Lys Glu Arg Glu Gly Lys Ser Glu Ile  
785 790 795 800

Ala Pro Ile Ser Glu Glu Leu Glu Arg Ile Val Leu Ala Met His  
805 810 815

Ile His Gln Gln Asn Ser His Met Glu Thr Lys Thr Arg Lys Asp Pro  
820 825 830

Lys Asp Ser Ile Leu Thr Arg Ala Gln Asn Met Leu Arg Lys Arg Ser  
835 840 845

Gly Tyr Ser Asn Leu Lys Asn Ala Glu Ser Val Glu Met Leu Asn Thr  
850 855 860

Leu  
865

<210> 25  
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<212> DNA  
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<220>  
<223> Sequencing primer for TOPO-pCRII: bases 434-458

<400> 25  
cgccagggtt ttcccagtca cgac

24

<210> 26  
<211> 17  
<212> DNA  
<213> artificial

<220>  
<223> M13 reverse sequencing primer for TOPO-pCRII: bases 205-222

<400> 26  
cagggaaacag ctatgac

17

<210> 27  
<211> 20  
<212> DNA  
<213> artificial

<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases 1989-2008

<400> 27  
cagggacgag aagaggctta

20

<210> 28  
<211> 19  
<212> DNA  
<213> artificial

<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases 1513-1531

<400> 28  
acaccagagc agctctatg

19

<210> 29  
<211> 24  
<212> DNA  
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<220>  
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2399-2422

<400> 29  
tagcaccaat cagtgaagaa gagc

24

<210> 30  
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<212> DNA  
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<220>  
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322-343

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gccagtgata tggcacacag tg

22

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<212> DNA  
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140-163

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taacagggtca ctatgaaaca cacg

24

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<211> 24  
<212> DNA  
<213> artificial

<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases  
537-560

<400> 32  
ttctttaaga ctaaacacag gtgg

24

<210> 33  
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<212> DNA  
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<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases  
815-835

<400> 33

ggagtggta agatgatcat g

21

<210> 34  
<211> 25  
<212> DNA  
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<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases  
993-1017

<400> 34  
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25

<210> 35  
<211> 21  
<212> DNA  
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<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases  
1073-1093

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21

<210> 36  
<211> 22  
<212> DNA  
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<220>  
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases  
1673-1694

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gatgcactga gaagcctgag ac

22

<210> 37  
<211> 823  
<212> PRT  
<213> Human herpesvirus 8

<400> 37  
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1 5 10 15

Val Cys Phe Cys Ala Gly Ala Ala His Ser Arg Gly Asp Thr Phe Gln  
20 25 30

Thr Ser Ser Ser Pro Thr Pro Pro Gly Ser Ser Ser Lys Ala Pro Thr  
35 40 45

Lys Pro Gly Glu Glu Ala Ser Gly Pro Lys Ser Val Asp Phe Tyr Gln  
 50 55 60

Phe Arg Val Cys Ser Ala Ser Ile Thr Gly Glu Leu Phe Arg Phe Asn  
 65 70 75 80

Leu Glu Gln Thr Cys Pro Asp Thr Lys Asp Lys Tyr His Gln Glu Gly  
 85 90 95

Ile Leu Leu Val Tyr Lys Lys Asn Ile Val Pro His Ile Phe Lys Val  
 100 105 110

Arg Arg Tyr Arg Lys Ile Ala Thr Ser Val Thr Val Tyr Arg Gly Leu  
 115 120 125

Thr Glu Ser Ala Ile Thr Asn Lys Tyr Glu Leu Pro Arg Pro Val Pro  
 130 135 140

Leu Tyr Glu Ile Ser His Met Asp Ser Thr Tyr Gln Cys Phe Ser Ser  
 145 150 155 160

Met Lys Val Asn Val Asn Gly Val Glu Asn Thr Phe Thr Asp Arg Asp  
 165 170 175

Asp Val Asn Thr Thr Val Phe Leu Gln Pro Val Glu Gly Leu Thr Asp  
 180 185 190

Asn Ile Gln Arg Tyr Phe Ser Gln Pro Val Ile Tyr Ala Glu Pro Gly  
 195 200 205

Trp Phe Pro Gly Ile Tyr Arg Val Arg Thr Thr Val Asn Cys Glu Ile  
 210 215 220

Val Asp Met Ile Ala Arg Ser Ala Glu Pro Tyr Asn Tyr Phe Val Thr  
 225 230 235 240

Ser Leu Gly Asp Thr Val Glu Val Ser Pro Phe Cys Tyr Asn Glu Ser  
 245 250 255

Ser Cys Ser Thr Thr Pro Ser Asn Lys Asn Gly Leu Ser Val Gln Val  
 260 265 270

Val Leu Asn His Thr Val Val Thr Tyr Ser Asp Arg Gly Thr Ser Pro  
 275 280 285

Thr Pro Gln Asn Arg Ile Phe Val Glu Thr Gly Ala Tyr Thr Leu Ser  
 290 295 300

Trp Ala Ser Glu Ser Lys Thr Thr Ala Val Cys Pro Leu Ala Leu Trp  
 305 310 315 320

Lys Thr Phe Pro Arg Ser Ile Gln Thr Thr His Glu Asp Ser Phe His  
 325 330 335

Phe Val Ala Asn Glu Ile Thr Ala Thr Phe Thr Ala Pro Leu Thr Pro  
 340 345 350

Val Ala Asn Phe Thr Asp Thr Tyr Ser Cys Leu Thr Ser Asp Ile Asn  
355 360 365

Thr Thr Leu Asn Ala Ser Lys Ala Lys Leu Ala Ser Thr His Val Pro  
370 375 380

Asn Gly Thr Val Gln Tyr Phe His Thr Thr Gly Gly Leu Tyr Leu Val  
385 390 395 400

Trp Gln Pro Met Ser Ala Ile Asn Leu Thr His Ala Gln Gly Asp Ser  
405 410 415

Gly Asn Pro Thr Ser Ser Pro Pro Pro Ser Ala Ser Pro Met Thr Thr  
420 425 430

Ser Ala Ser Arg Arg Lys Arg Arg Ser Ala Ser Thr Ala Ala Ala Gly  
435 440 445

Gly Gly Gly Ser Thr Asp Asn Leu Ser Tyr Thr Gln Leu Gln Phe Ala  
450 455 460

Tyr Asp Lys Leu Arg Asp Gly Ile Asn Gln Val Leu Glu Glu Leu Ser  
465 470 475 480

Arg Ala Trp Cys Arg Glu Gln Val Arg Asp Asn Leu Met Trp Tyr Glu  
485 490 495

Leu Ser Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly Arg  
500 505 510

Pro Val Ser Ala Lys Phe Val Gly Asp Ala Ile Ser Val Thr Glu Cys  
515 520 525

Ile Asn Val Asp Gln Ser Ser Val Asn Ile His Lys Ser Leu Arg Thr  
530 535 540

Asn Ser Lys Asp Val Cys Tyr Ala Arg Pro Leu Val Thr Phe Lys Phe  
545 550 555 560

Leu Asn Ser Ser Asn Leu Phe Thr Gly Gln Leu Gly Ala Arg Asn Glu  
565 570 575

Ile Ile Leu Thr Asn Asn Gln Val Glu Thr Cys Lys Asp Thr Cys Glu  
580 585 590

His Tyr Phe Ile Thr Arg Asn Glu Thr Leu Val Tyr Lys Asp Tyr Ala  
595 600 605

Tyr Leu Arg Thr Ile Asn Thr Thr Asp Ile Ser Thr Leu Asn Thr Phe  
610 615 620

Ile Ala Leu Asn Leu Ser Phe Ile Gln Asn Ile Asp Phe Lys Ala Ile  
625 630 635 640

Glu Leu Tyr Ser Ser Ala Glu Lys Arg Leu Ala Ser Ser Val Phe Asp  
645 650 655

Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr His Arg Leu Ala  
660 665 670

Gly Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Met Asn Lys Glu Arg  
675 680 685

Phe Val Arg Asp Leu Ser Glu Ile Val Ala Asp Leu Gly Gly Ile Gly  
690 695 700

Lys Thr Val Val Asn Val Ala Ser Ser Val Val Thr Leu Cys Gly Ser  
705 710 715 720

Leu Val Thr Gly Phe Ile Asn Phe Ile Lys His Pro Leu Gly Gly Met  
725 730 735

Leu Met Ile Ile Ile Val Ile Ala Ile Ile Leu Ile Ile Phe Met Leu  
740 745 750

Ser Arg Arg Thr Asn Thr Ile Ala Gln Ala Pro Val Lys Met Ile Tyr  
755 760 765

Pro Asp Val Asp Arg Arg Ala Pro Pro Ser Gly Gly Ala Pro Thr Arg  
770 775 780

Glu Glu Ile Lys Asn Ile Leu Leu Gly Met His Gln Leu Gln Gln Glu  
785 790 795 800

Arg Gln Lys Ala Asp Asp Leu Lys Lys Ser Thr Pro Ser Val Phe Gln  
805 810 815

Arg Thr Ala Asn Gly Leu Arg  
820

<210> 38

<211> 808

<212> PRT

<213> Rhesus monkey rhadinovirus

<400> 38

Met Met Ile Thr Asn Arg Thr Arg Arg Leu Leu Arg Ala Trp Val Val  
1 5 10 15

Ile Ile Ala Ile Gly Thr Ala Val Gly Glu Asn Val Thr Thr Pro Lys  
20 25 30

Gly Ala Thr Thr Ala Lys Pro Thr Pro Gly Pro Ser Thr Pro Thr  
35 40 45

Pro Pro Glu Asn Pro Pro Arg Ala Glu Ala Phe Lys Phe Arg Val Cys  
50 55 60

Ser Ala Ser Ala Thr Gly Glu Leu Phe Arg Phe Asn Leu Glu Lys Thr  
65 70 75 80

Cys Pro Gly Thr Glu Asp Lys Thr His Gln Glu Gly Ile Leu Met Val  
85 90 95

Phe Lys Lys Asn Ile Val Pro His Ile Phe Lys Val Arg Arg Tyr Arg  
 100 105 110  
 Lys Val Ala Thr Ser Val Thr Val Tyr Arg Gly Trp Thr Glu Thr Ala  
 115 120 125  
 Val Thr Gly Lys Gln Glu Val Ile Arg Pro Val Pro Gln Tyr Glu Ile  
 130 135 140  
 Asn His Met Asp Thr Thr Tyr Gln Cys Phe Ser Ser Met Arg Val Asn  
 145 150 155 160  
 Val Asn Gly Ile Val Asn Thr Tyr Thr Asp Arg Asp Phe Thr Asn Gln  
 165 170 175  
 Thr Val Phe Leu Gln Pro Val Glu Gly Leu Thr Asp Asn Ile Gln Arg  
 180 185 190  
 Tyr Phe Ser Gln Pro Val Leu Tyr Thr Pro Gly Trp Phe Pro Gly  
 195 200 205  
 Ile Tyr Arg Val Arg Thr Thr Val Asn Cys Glu Ile Val Asp Met Ile  
 210 215 220  
 Ala Arg Ser Ala Glu Pro Tyr Ser Tyr Phe Val Thr Ala Leu Gly Asp  
 225 230 235 240  
 Thr Val Glu Val Ser Pro Phe Cys His Asn Asp Ser Thr Cys Ser Val  
 245 250 255  
 Ala Glu Lys Thr Glu Asn Gly Leu Gly Ala Arg Val Leu Thr Asn Tyr  
 260 265 270  
 Thr Met Val Asp Phe Ala Thr Arg Ala Pro Thr Thr Glu Thr Arg Val  
 275 280 285  
 Phe Ala Asp Ser Gly Glu Tyr Thr Val Ser Trp Lys Ala Glu Asp Pro  
 290 295 300  
 Lys Ser Ala Val Cys Ala Leu Thr Leu Trp Lys Thr Phe Pro Arg Ala  
 305 310 315 320  
 Ile Gln Thr Thr His Glu Ala Ser Tyr His Phe Val Ala Asn Asp Val  
 325 330 335  
 Thr Ala Thr Phe Thr Ser Pro Leu Ser Glu Val Ala Asn Phe Thr Gly  
 340 345 350  
 Thr Tyr Ser Cys Leu Asp Glu Val Ile Gln Lys Thr Leu Asn Asp Thr  
 355 360 365  
 Ile Lys Lys Leu Ser Asp Thr His Val Thr Asn Gly Ser Ala Gln Tyr  
 370 375 380  
 Tyr Lys Thr Glu Gly Leu Phe Leu Leu Trp Gln Pro Leu Thr Pro  
 385 390 395 400

Leu Ser Leu Val Asp Glu Met Arg Gly Leu Asn Gly Thr Thr Pro Ala  
                   405                  410                  415  
  
 Pro Pro Ala Thr Thr Ser Thr Val Ser Arg Val Arg Arg Ser Val Asn  
                   420                  425                  430  
  
 Thr Asn Glu Gln Ala Thr Asp Asn Leu Ala Ala Pro Gln Leu Gln Phe  
                   435                  440                  445  
  
 Ala Tyr Asp Lys Leu Arg Ala Ser Ile Asn Lys Val Leu Glu Glu Leu  
                   450                  455                  460  
  
 Ser Arg Ala Trp Cys Arg Glu Gln Val Arg Asp Thr Tyr Met Trp Tyr  
                   465                  470                  475                  480  
  
 Glu Leu Ser Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly  
                   485                  490                  495  
  
 Arg Pro Val Ser Ala Lys Phe Val Gly Asp Ala Ile Ser Val Thr Asp  
                   500                  505                  510  
  
 Cys Val Ala Val Asp Gln Ala Ser Val Ser Ile His Lys Ser Leu Arg  
                   515                  520                  525  
  
 Thr Ser Thr Pro Gly Met Cys Tyr Ser Arg Pro Pro Val Thr Phe Arg  
                   530                  535                  540  
  
 Phe Leu Asn Ser Thr Thr Leu Phe Lys Gly Gln Leu Gly Pro Arg Asn  
                   545                  550                  555                  560  
  
 Glu Ile Ile Leu Thr Asp Asn Gln Val Glu Ala Cys Lys Glu Thr Cys  
                   565                  570                  575  
  
 Glu His Tyr Phe Ile Ala Ser Asn Val Thr Tyr Tyr Tyr Lys Asp Tyr  
                   580                  585                  590  
  
 Val Phe Val Lys Lys Ile Asn Thr Ser Glu Ile Ser Thr Leu Gly Thr  
                   595                  600                  605  
  
 Phe Ile Ala Leu Asn Leu Ser Phe Ile Glu Asn Ile Asp Phe Arg Val  
                   610                  615                  620  
  
 Ile Glu Leu Tyr Ser Arg Ala Glu Lys Lys Leu Ser Gly Ser Val Phe  
                   625                  630                  635                  640  
  
 Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Leu  
                   645                  650                  655  
  
 Ala Gly Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Leu Asn Arg Asp  
                   660                  665                  670  
  
 Arg Leu Ala Arg Asp Leu Ser Glu Ile Val Ala Asp Leu Gly Asp Val  
                   675                  680                  685  
  
 Gly Arg Thr Val Val Asn Val Ala Ser Ser Val Ile Thr Leu Phe Gly  
                   690                  695                  700

Ser Ile Val Ser Gly Phe Ile Asn Phe Ile Lys Ser Pro Phe Gly Gly  
705 710 715 720

Met Leu Met Ile Leu Val Ile Val Ala Val Val Leu Ile Val Phe Ala  
725 730 735

Leu Asn Arg Arg Thr Asn Ala Ile Ala Gln Ala Pro Ile Arg Met Ile  
740 745 750

Tyr Pro Asp Ile Asp Lys Met Gln Pro Ser Gly Gly Lys Val Asp Gln  
755 760 765

Glu Gln Ile Lys Asn Ile Leu Ala Gly Met His Gln Leu Gln Gln Glu  
770 775 780

Glu Arg Arg Arg Leu Asp Glu Gln Gln Arg Ser Ala Pro Ser Leu Phe  
785 790 795 800

Arg Arg Ala Ser Asp Gly Leu Lys  
805

<210> 39

<211> 831

<212> PRT

<213> Murine herpesvirus 68

<400> 39

Met Tyr Pro Thr Val Lys Ser Met Arg Val Ala His Leu Thr Asn Leu  
1 5 10 15

Leu Thr Leu Leu Cys Leu Leu Cys His Thr His Leu Tyr Val Cys Gln  
20 25 30

Pro Thr Thr Leu Arg Gln Pro Ser Asp Met Thr Pro Ala Gln Asp Ala  
35 40 45

Pro Thr Glu Thr Pro Pro Pro Leu Ser Thr Asn Thr Asn Arg Gly Phe  
50 55 60

Glu Tyr Phe Arg Val Cys Gly Val Ala Ala Thr Gly Glu Thr Phe Arg  
65 70 75 80

Phe Asp Leu Asp Lys Thr Cys Pro Ser Thr Gln Asp Lys Lys His Val  
85 90 95

Glu Gly Ile Leu Leu Val Tyr Lys Ile Asn Ile Val Pro Tyr Ile Phe  
100 105 110

Lys Ile Arg Arg Tyr Arg Lys Ile Ile Thr Gln Leu Thr Ile Trp Arg  
115 120 125

Gly Leu Thr Thr Ser Ser Val Thr Gly Lys Phe Glu Met Ala Thr Gln  
130 135 140

Ala His Glu Trp Glu Val Gly Asp Phe Asp Ser Ile Tyr Gln Cys Tyr  
145 150 155 160

Asn Ser Ala Thr Met Val Val Asn Asn Val Arg Gln Val Tyr Val Asp			
165	170	175	
Arg Asp Gly Val Asn Lys Thr Val Asn Ile Arg Pro Val Asp Gly Leu			
180	185	190	
Thr Gly Asn Ile Gln Arg Tyr Phe Ser Gln Pro Thr Leu Tyr Ser Glu			
195	200	205	
Pro Gly Trp Met Pro Gly Phe Tyr Arg Val Arg Thr Thr Val Asn Cys			
210	215	220	
Glu Ile Val Asp Met Val Ala Arg Ser Met Asp Pro Tyr Asn Tyr Ile			
225	230	235	240
Ala Thr Ala Leu Gly Asp Ser Leu Glu Leu Ser Pro Phe Gln Thr Phe			
245	250	255	
Asp Asn Thr Ser Gln Ser Thr Ala Pro Lys Arg Ala Asp Met Arg Val			
260	265	270	
Arg Glu Val Lys Asn Tyr Lys Phe Val Asp Tyr Asn Asn Arg Gly Thr			
275	280	285	
Ala Pro Ala Gly Gln Ser Arg Thr Phe Leu Glu Thr Pro Ser Ala Thr			
290	295	300	
Tyr Ser Trp Lys Thr Ala Thr Arg Gln Thr Ala Thr Cys Asp Leu Val			
305	310	315	320
His Trp Lys Thr Phe Pro Arg Ala Ile Gln Thr Ala His Glu His Ser			
325	330	335	
Tyr His Phe Val Ala Asn Glu Val Thr Ala Thr Phe Asn Thr Pro Leu			
340	345	350	
Thr Glu Val Glu Asn Phe Thr Ser Thr Tyr Ser Cys Val Ser Asp Gln			
355	360	365	
Ile Asn Lys Thr Ile Ser Glu Tyr Ile Gln Lys Leu Asn Asn Ser Tyr			
370	375	380	
Val Ala Ser Gly Lys Thr Gln Tyr Phe Lys Thr Asp Gly Asn Leu Tyr			
385	390	395	400
Leu Ile Trp Gln Pro Leu Glu His Pro Glu Ile Glu Asp Ile Asp Glu			
405	410	415	
Asp Ser Asp Pro Glu Pro Thr Pro Ala Pro Pro Lys Ser Thr Arg Arg			
420	425	430	
Lys Arg Glu Ala Ala Asp Asn Gly Asn Ser Thr Ser Glu Val Ser Lys			
435	440	445	
Gly Ser Glu Asn Pro Leu Ile Thr Ala Gln Ile Gln Phe Ala Tyr Asp			
450	455	460	

Lys Leu Thr Thr Ser Val Asn Asn Val Leu Glu Glu Leu Ser Arg Ala  
 465 470 475 480  
 Trp Cys Arg Glu Gln Val Arg Asp Thr Leu Met Trp Tyr Glu Leu Ser  
 485 490 495  
 Lys Val Asn Pro Thr Ser Val Met Ser Ala Ile Tyr Gly Lys Pro Val  
 500 505 510  
 Ala Ala Arg Tyr Val Gly Asp Ala Ile Ser Val Thr Asp Cys Ile Tyr  
 515 520 525  
 Val Asp Gln Ser Ser Val Asn Ile His Gln Ser Leu Arg Leu Gln His  
 530 535 540  
 Asp Lys Thr Thr Cys Tyr Ser Arg Pro Arg Val Thr Phe Lys Phe Ile  
 545 550 555 560  
 Asn Ser Thr Asp Pro Leu Thr Gly Gln Leu Gly Pro Arg Lys Glu Ile  
 565 570 575  
 Ile Leu Ser Asn Thr Asn Ile Glu Thr Cys Lys Asp Glu Ser Glu His  
 580 585 590  
 Tyr Phe Ile Val Gly Glu Tyr Ile Tyr Tyr Tyr Lys Asn Tyr Ile Phe  
 595 600 605  
 Glu Glu Lys Leu Asn Leu Ser Ser Ile Ala Thr Leu Asp Thr Phe Ile  
 610 615 620  
 Ala Leu Asn Ile Ser Phe Ile Glu Asn Ile Asp Phe Lys Thr Val Glu  
 625 630 635 640  
 Leu Tyr Ser Ser Thr Glu Arg Lys Leu Ala Ser Ser Val Phe Asp Ile  
 645 650 655  
 Glu Ser Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Tyr Ser Leu Ala Gly  
 660 665 670  
 Ile Lys Lys Asp Leu Asp Asn Thr Ile Asp Tyr Asn Arg Asp Arg Leu  
 675 680 685  
 Val Gln Asp Leu Ser Asp Met Met Ala Asp Leu Gly Asp Ile Gly Arg  
 690 695 700  
 Ser Val Val Asn Val Val Ser Ser Val Val Thr Phe Phe Ser Ser Ile  
 705 710 715 720  
 Val Thr Gly Phe Ile Lys Phe Phe Thr Asn Pro Leu Gly Gly Ile Phe  
 725 730 735  
 Ile Leu Leu Ile Ile Gly Gly Ile Ile Phe Leu Val Val Val Leu Asn  
 740 745 750  
 Arg Arg Asn Ser Gln Phe His Asp Ala Pro Ile Lys Met Leu Tyr Pro  
 755 760 765

Ser Val Glu Asn Tyr Ala Ala Arg Gln Ala Pro Pro Pro Tyr Ser Ala  
 770 775 780  
 Ser Pro Pro Ala Ile Asp Lys Glu Glu Ile Lys Arg Ile Leu Leu Gly  
 785 790 795 800  
 Met His Gln Val His Gln Glu Glu Lys Glu Ala Gln Lys Gln Leu Thr  
 805 810 815  
 Asn Ser Gly Pro Thr Leu Trp Gln Lys Ala Thr Gly Phe Leu Arg  
 820 825 830  
 <210> 40  
 <211> 844  
 <212> PRT  
 <213> Bovine herpesvirus 4  
 <400> 40  
 Tyr Tyr Lys Thr Ile Leu Phe Phe Ala Leu Ile Lys Val Cys Ser Phe  
 1 5 10 15  
 Asn Gln Thr Thr His Ser Thr Thr Ser Pro Ser Ile Ser Ser  
 20 25 30  
 Thr Thr Ser Ser Thr Thr Ser Thr Ser Lys Pro Ser Asn Thr Thr  
 35 40 45  
 Ser Thr Asn Ser Ser Leu Ala Ala Ser Pro Gln Asn Thr Ser Thr Ser  
 50 55 60  
 Lys Pro Ser Thr Asp Asn Gln Gly Thr Ser Thr Pro Thr Ile Pro Thr  
 65 70 75 80  
 Val Thr Asp Asp Thr Ala Ser Lys Asn Phe Tyr Lys Tyr Arg Val Cys  
 85 90 95  
 Ser Ala Ser Ser Ser Gly Glu Leu Phe Arg Phe Asp Leu Asp Gln  
 100 105 110  
 Thr Cys Pro Asp Thr Lys Asp Lys Lys His Val Glu Gly Ile Leu Leu  
 115 120 125  
 Val Leu Lys Lys Asn Ile Val Pro Tyr Ile Phe Lys Val Arg Lys Tyr  
 130 135 140  
 Arg Lys Ile Ala Thr Ser Val Thr Val Tyr Arg Gly Trp Ser Gln Ala  
 145 150 155 160  
 Ala Val Thr Asn Arg Asp Asp Ile Ser Arg Ala Ile Pro Tyr Asn Glu  
 165 170 175  
 Ile Ser Met Ile Asp Arg Thr Tyr His Cys Phe Ser Ala Met Ala Thr  
 180 185 190  
 Val Ile Asn Gly Ile Leu Asn Thr Tyr Ile Asp Arg Asp Ser Glu Asn  
 195 200 205

Lys Ser Val Pro Leu Gln Pro Val Ala Gly Leu Thr Glu Asn Ile Asn  
 210 215 220  
 Arg Tyr Phe Ser Gln Pro Leu Ile Tyr Ala Glu Pro Gly Trp Phe Pro  
 225 230 235 240  
 Gly Ile Tyr Arg Val Arg Thr Thr Val Asn Cys Glu Val Val Asp Met  
 245 250 255  
 Tyr Ala Arg Ser Val Glu Pro Tyr Thr His Phe Ile Thr Ala Leu Gly  
 260 265 270  
 Asp Thr Ile Glu Ile Ser Pro Phe Cys His Asn Asn Ser Gln Cys Thr  
 275 280 285  
 Thr Gly Asn Ser Thr Ser Arg Asp Ala Thr Lys Val Trp Ile Glu Glu  
 290 295 300  
 Asn His Gln Thr Val Asp Tyr Glu Arg Arg Gly His Pro Thr Lys Asp  
 305 310 315 320  
 Lys Arg Ile Phe Leu Lys Asp Glu Glu Tyr Thr Ile Ser Trp Lys Ala  
 325 330 335  
 Glu Asp Arg Glu Arg Ala Ile Cys Asp Phe Val Ile Trp Lys Thr Phe  
 340 345 350  
 Pro Arg Ala Ile Gln Thr Ile His Asn Glu Ser Phe His Phe Val Ala  
 355 360 365  
 Asn Glu Val Thr Ala Ser Phe Leu Thr Ser Asn Gln Glu Glu Thr Glu  
 370 375 380  
 Leu Arg Gly Asn Thr Glu Ile Leu Asn Cys Met Asn Ser Thr Ile Asn  
 385 390 395 400  
 Glu Thr Leu Glu Glu Thr Val Lys Lys Phe Asn Lys Ser His Ile Arg  
 405 410 415  
 Asp Gly Glu Val Lys Tyr Tyr Lys Thr Asn Gly Gly Leu Phe Leu Ile  
 420 425 430  
 Trp Gln Ala Met Lys Pro Leu Asn Leu Ser Glu His Thr Asn Tyr Thr  
 435 440 445  
 Ile Glu Arg Asn Asn Lys Thr Gly Asn Lys Ser Arg Gln Lys Arg Ser  
 450 455 460  
 Val Asp Thr Lys Thr Phe Gln Gly Ala Lys Gly Leu Ser Thr Ala Gln  
 465 470 475 480  
 Val Gln Tyr Ala Tyr Asp His Leu Arg Thr Ser Met Asn His Ile Leu  
 485 490 495  
 Glu Glu Leu Thr Lys Thr Trp Cys Arg Glu Gln Lys Lys Asp Asn Leu  
 500 505 510

Met Trp Tyr Glu Leu Ser Lys Ile Asn Pro Val Ser Val Met Ala Ala  
 515 520 525  
 Ile Tyr Gly Lys Pro Val Ala Val Lys Ala Met Gly Asp Ala Phe Met  
 530 535 540  
 Val Ser Glu Cys Ile Asn Val Asp Gln Ala Ser Val Asn Ile His Lys  
 545 550 555 560  
 Ser Met Arg Thr Asp Asp Pro Lys Val Cys Tyr Ser Arg Pro Leu Val  
 565 570 575  
 Thr Phe Lys Phe Val Asn Ser Thr Ala Thr Phe Arg Gly Gln Leu Gly  
 580 585 590  
 Thr Arg Asn Glu Ile Leu Leu Thr Asn Thr His Val Glu Thr Cys Arg  
 595 600 605  
 Pro Thr Ala Asp His Tyr Phe Phe Val Lys Asn Met Thr His Tyr Phe  
 610 615 620  
 Lys Asp Tyr Lys Phe Val Lys Thr Met Asp Thr Asn Asn Ile Ser Thr  
 625 630 635 640  
 Leu Asp Thr Phe Leu Thr Leu Asn Leu Thr Phe Ile Asp Asn Ile Asp  
 645 650 655  
 Phe Lys Thr Val Glu Leu Tyr Ser Glu Thr Glu Arg Lys Met Ala Ser  
 660 665 670  
 Ala Leu Asp Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln  
 675 680 685  
 Lys Leu Ala Ser Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Leu Asn  
 690 695 700  
 Arg Asp Arg Leu Val Lys Asp Leu Ser Glu Met Met Ala Asp Leu Gly  
 705 710 715 720  
 Asp Ile Gly Lys Val Val Val Asn Thr Phe Ser Gly Ile Val Thr Val  
 725 730 735  
 Phe Gly Ser Ile Val Gly Phe Val Ser Phe Phe Thr Asn Pro Ile  
 740 745 750  
 Gly Gly Val Thr Ile Ile Leu Leu Leu Ile Val Val Val Phe Val Val  
 755 760 765  
 Phe Ile Val Ser Arg Arg Thr Asn Asn Met Asn Glu Ala Pro Ile Lys  
 770 775 780  
 Met Ile Tyr Pro Asn Ile Asp Lys Ala Ser Glu Gln Glu Asn Ile Gln  
 785 790 795 800  
 Pro Leu Pro Gly Glu Glu Ile Lys Arg Ile Leu Leu Gly Met His Gln  
 805 810 815

Leu Gln Gln Ser Glu His Gly Lys Ser Glu Glu Glu Ala Ser His Lys  
820 825 830

Pro Gly Leu Phe Gln Leu Leu Gly Asp Gly Leu Gln  
835 840

<210> 41  
<211> 791  
<212> PRT  
<213> Ateline herpesvirus 3

<400> 41  
Met Thr Leu Asn Arg Cys Val Leu Leu Ile Val Leu Thr Phe Ser Thr  
1 5 10 15

Ala Cys Ser Gln Thr Thr Pro Ala Ser Ser Asp Glu Asn Gly Lys Thr  
20 25 30

Pro Ala Ile Glu Lys Glu Tyr Phe Lys Tyr Arg Val Cys Ser Ala Ser  
35 40 45

Thr Thr Gly Glu Leu Phe Arg Phe Asn Leu Asp Arg Ala Cys Pro Ser  
50 55 60

Thr Glu Asp Lys Val His Arg Glu Gly Ile Leu Leu Val Tyr Lys Lys  
65 70 75 80

Asn Ile Val Pro His Ile Phe Lys Val Arg Arg Tyr Lys Lys Ile Ala  
85 90 95

Thr Ser Val Arg Ile Phe Asn Gly Trp Ser Arg Glu Gly Val Ala Ile  
100 105 110

Thr Asn Lys Trp Glu Leu Ser Arg Ala Val Pro Lys Tyr Glu Ile Asn  
115 120 125

Leu Met Asp Lys Asn Tyr Gln Cys His Asn Cys Met Gln Ile Glu Val  
130 135 140

Asn Gly Leu Leu Asn Ser Tyr Cys Asp Arg Asp Gly Asn Asn Lys Thr  
145 150 155 160

Val Asp Leu Lys Pro Val Asp Gly Leu Thr Gly Ala Ile Thr Arg Tyr  
165 170 175

Val Ser Gln Pro Lys Ile Phe Ala Asp Ala Gly Trp Leu Trp Gly Thr  
180 185 190

Tyr Lys Thr Arg Thr Val Asn Cys Glu Ile Val Glu Met Phe Ala  
195 200 205

Arg Ser Ala Asp Pro Tyr Thr Tyr Phe Val Thr Ala Leu Gly Asp Thr  
210 215 220

Val Glu Val Ser Pro Phe Cys Asp Ala Glu Asn Ser Cys Pro Asn Ala  
225 230 235 240

Ser Asp Val Leu Ser Ser Gln Val Asp Phe Asn His Thr Val Val Asp  
                   245                  250                  255  
  
 Tyr Gly Asn Arg Ala Thr Ser Gln Gln His Gly Lys Arg Ile Phe Ala  
                   260                  265                  270  
  
 His Thr Leu Asp Tyr Ser Val Ser Trp Glu Ala Ile Asn Lys Thr Thr  
                   275                  280                  285  
  
 Ser Val Cys Ser Met Val Phe Trp Lys Gly Phe Gln Arg Ala Ile Gln  
                   290                  295                  300  
  
 Thr Glu His Asp Ser Thr Tyr His Phe Ile Ala Asn Glu Ile Thr Ala  
                   305                  310                  315                  320  
  
 Gly Phe Ser Thr Ser Lys Glu Thr Leu Ala Ser Phe Ser Ser Glu Tyr  
                   325                  330                  335  
  
 Ser Cys Leu Met Ser Asp Ile Asn Ser Thr Leu Thr Asp Lys Ile Gly  
                   340                  345                  350  
  
 Arg Val Asn Asn Thr His Val Pro Asn Gly Thr Ala Gln Tyr Phe Lys  
                   355                  360                  365  
  
 Thr Glu Gly Gly Met Ile Leu Val Trp Gln Pro Leu Thr Ala Ile Glu  
                   370                  375                  380  
  
 Leu Glu Glu Ala Met Ile Glu Ala Thr Thr Val Ser Pro Thr Pro Leu  
                   385                  390                  395                  400  
  
 Ser Thr Ala His Leu Thr Ser Arg Arg Thr Gly Arg Arg Lys Arg Asp  
                   405                  410                  415  
  
 Val Ser Ala Gly Ser Glu Asn Ser Val Leu Leu Ala Gln Ile Gln Tyr  
                   420                  425                  430  
  
 Ala Tyr Asp Lys Leu Arg Gln Ser Ile Asn Asn Val Leu Glu Glu Leu  
                   435                  440                  445  
  
 Ala Ile Thr Trp Cys Arg Glu Gln Val Arg Gln Thr Met Ile Trp Tyr  
                   450                  455                  460  
  
 Glu Ile Ala Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly  
                   465                  470                  475                  480  
  
 Lys Pro Val Ser Ala Lys Ala Leu Gly Asp Val Ile Ser Val Thr Glu  
                   485                  490                  495  
  
 Cys Ile Asn Val Asp Gln Thr Ser Val Ser Ile His Lys Ser Leu Lys  
                   500                  505                  510  
  
 Thr Thr Asn Asn Asp Val Cys Tyr Ser Arg Pro Pro Val Thr Phe Lys  
                   515                  520                  525  
  
 Phe Val Asn Ser Ser Gln Leu Phe Lys Gly Gln Leu Gly Ala Arg Asn  
                   530                  535                  540

Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn Ala  
 545 550 555 560  
 Glu His Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn Tyr  
 565 570 575  
 Leu His Val Glu Thr Leu Pro Leu Thr Asn Ile Ser Thr Leu Asp Thr  
 580 585 590  
 Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys Ala  
 595 600 605  
 Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe Asp  
 610 615 620  
 Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile Ser  
 625 630 635 640  
 Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp Arg  
 645 650 655  
 Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile Gly  
 660 665 670  
 Lys Val Ile Val Asn Ile Ala Ser Ser Ala Phe Ser Leu Phe Gly Gly  
 675 680 685  
 Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly Met  
 690 695 700  
 Leu Thr Phe Leu Leu Val Gly Ala Ile Ile Leu Val Ile Leu Leu  
 705 710 715 720  
 Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile Tyr  
 725 730 735  
 Pro Asp Ile Glu Lys Ser Arg Ser Ser Val Thr Pro Thr Glu Pro Glu  
 740 745 750  
 Val Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu Glu  
 755 760 765  
 Tyr Lys Lys Arg Glu Glu His Lys Ala Ser Gln Pro Ser Phe Leu Lys  
 770 775 780  
 Arg Ala Thr Asp Ala Phe Leu  
 785 790  
 <210> 42  
 <211> 792  
 <212> PRT  
 <213> Herpesvirus saimiri  
 <400> 42  
 Met Val Pro Asn Lys His Leu Leu Ile Ile Leu Ser Phe Ser Thr  
 1 5 10 15

Ala Cys Gly Gln Thr Thr Pro Thr Thr Ala Val Glu Lys Asn Lys Thr  
           20                     25                     30

Gln Ala Ile Tyr Gln Glu Tyr Phe Lys Tyr Arg Val Cys Ser Ala Ser  
           35                     40                     45

Thr Thr Gly Glu Leu Phe Arg Phe Asp Leu Asp Arg Thr Cys Pro Ser  
           50                     55                     60

Thr Glu Asp Lys Val His Lys Glu Gly Ile Leu Leu Val Tyr Lys Lys  
   65                     70                     75                     80

Asn Ile Val Pro Tyr Ile Phe Lys Val Arg Arg Tyr Lys Lys Ile Thr  
   85                     90                     95

Thr Ser Val Arg Ile Phe Asn Gly Trp Thr Arg Glu Gly Val Ala Ile  
   100                     105                     110

Thr Asn Lys Trp Glu Leu Ser Arg Ala Val Pro Lys Tyr Glu Ile Asp  
   115                     120                     125

Ile Met Asp Lys Thr Tyr Gln Cys His Asn Cys Met Gln Ile Glu Val  
   130                     135                     140

Asn Gly Met Leu Asn Ser Tyr Tyr Asp Arg Asp Gly Asn Asn Lys Thr  
   145                     150                     155                     160

Val Asp Leu Lys Pro Val Asp Gly Leu Thr Gly Ala Ile Thr Arg Tyr  
   165                     170                     175

Ile Ser Gln Pro Lys Val Phe Ala Asp Pro Gly Trp Leu Trp Gly Thr  
   180                     185                     190

Tyr Arg Thr Arg Thr Val Asn Cys Glu Ile Val Asp Met Phe Ala  
   195                     200                     205

Arg Ser Ala Asp Pro Tyr Thr Tyr Phe Val Thr Ala Leu Gly Asp Thr  
   210                     215                     220

Val Glu Val Ser Pro Phe Cys Asp Val Asp Asn Ser Cys Pro Asn Ala  
   225                     230                     235                     240

Thr Asp Val Leu Ser Val Gln Ile Asp Leu Asn His Thr Val Val Asp  
   245                     250                     255

Tyr Gly Asn Arg Ala Thr Ser Gln Gln His Lys Lys Arg Ile Phe Ala  
   260                     265                     270

His Thr Leu Asp Tyr Ser Val Ser Trp Glu Ala Val Asn Lys Ser Ala  
   275                     280                     285

Ser Val Cys Ser Met Val Phe Trp Lys Ser Phe Gln Arg Ala Ile Gln  
   290                     295                     300

Thr Glu His Asp Leu Thr Tyr His Phe Ile Ala Asn Glu Ile Thr Ala  
   305                     310                     315                     320

Gly Phe Ser Thr Val Lys Glu Pro Leu Ala Asn Phe Thr Ser Asp Tyr  
                   325                  330                  335  
  
 Asn Cys Leu Met Thr His Ile Asn Thr Thr Leu Glu Asp Lys Ile Ala  
                   340                  345                  350  
  
 Arg Val Asn Asn Thr His Thr Pro Asn Gly Thr Ala Glu Tyr Tyr Gln  
                   355                  360                  365  
  
 Thr Glu Gly Gly Met Ile Leu Val Trp Gln Pro Leu Ile Ala Ile Glu  
                   370                  375                  380  
  
 Leu Glu Glu Ala Met Leu Glu Ala Thr Thr Ser Pro Val Thr Pro Ser  
                   385                  390                  395                  400  
  
 Ala Pro Thr Ser Ser Arg Ser Lys Arg Ala Ile Arg Ser Ile Arg  
                   405                  410                  415  
  
 Asp Val Ser Ala Gly Ser Glu Asn Asn Val Phe Leu Ser Gln Ile Gln  
                   420                  425                  430  
  
 Tyr Ala Tyr Asp Lys Leu Arg Gln Ser Ile Asn Asn Val Leu Glu Glu  
                   435                  440                  445  
  
 Leu Ala Ile Thr Trp Cys Arg Glu Gln Val Arg Gln Thr Met Val Trp  
                   450                  455                  460  
  
 Tyr Glu Ile Ala Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr  
                   465                  470                  475                  480  
  
 Gly Lys Pro Val Ser Arg Lys Ala Leu Gly Asp Val Ile Ser Val Thr  
                   485                  490                  495  
  
 Glu Cys Ile Asn Val Asp Gln Ser Ser Val Ser Ile His Lys Ser Leu  
                   500                  505                  510  
  
 Lys Thr Glu Asn Asn Asp Ile Cys Tyr Ser Arg Pro Pro Val Thr Phe  
                   515                  520                  525  
  
 Lys Phe Val Asn Ser Ser Gln Leu Phe Lys Gly Gln Leu Gly Ala Arg  
                   530                  535                  540  
  
 Asn Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn  
                   545                  550                  555                  560  
  
 Ala Glu Thr Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn  
                   565                  570                  575  
  
 Tyr Val His Val Glu Thr Leu Pro Val Asn Asn Ile Ser Thr Leu Asp  
                   580                  585                  590  
  
 Thr Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys  
                   595                  600                  605  
  
 Ala Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe  
                   610                  615                  620

Asp Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile  
 625 630 635 640  
 Ser Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp  
 645 650 655  
 Arg Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile  
 660 665 670  
 Gly Lys Val Ile Val Asn Val Ala Ser Gly Ala Phe Ser Leu Phe Gly  
 675 680 685  
 Gly Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly  
 690 695 700  
 Met Phe Thr Phe Leu Leu Ile Gly Ala Val Ile Ile Leu Val Ile Leu  
 705 710 715 720  
 Leu Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile  
 725 730 735  
 Tyr Pro Asp Val Glu Lys Ser Lys Ser Thr Val Thr Pro Met Glu Pro  
 740 745 750  
 Glu Thr Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu  
 755 760 765  
 Ala Tyr Lys Lys Glu Glu Gln Arg Ala Ala Arg Pro Ser Ile Phe  
 770 775 780  
 Arg Gln Ala Ala Glu Thr Phe Leu  
 785 790  
 <210> 43  
 <211> 824  
 <212> PRT  
 <213> Equequine herpesvirus 2  
 <400> 43  
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 Ala Ala Leu Leu Cys Gln Gly Val Ala Gln Glu Val Val Ala Glu Thr  
 20 25 30  
 Thr Thr Pro Phe Ala Thr His Arg Pro Glu Val Val Ala Glu Glu Asn  
 35 40 45  
 Pro Ala Asn Pro Phe Leu Pro Phe Arg Val Cys Gly Ala Ser Pro Thr  
 50 55 60  
 Gly Gly Glu Ile Phe Arg Phe Pro Leu Glu Glu Ser Cys Pro Asn Thr  
 65 70 75 80  
 Glu Asp Lys Asp His Ile Glu Gly Ile Ala Leu Ile Tyr Lys Thr Asn  
 85 90 95

Ile Val Pro Tyr Val Phe Asn Val Arg Lys Tyr Arg Lys Ile Met Thr  
 100 105 110  
 Ser Thr Thr Ile Tyr Lys Gly Trp Ser Glu Asp Ala Ile Thr Asn Gln  
 115 120 125  
 His Thr Arg Ser Tyr Ala Val Pro Leu Tyr Glu Val Gln Met Met Asp  
 130 135 140  
 His Tyr Tyr Gln Cys Phe Ser Ala Val Gln Val Asn Glu Gly Gly His  
 145 150 155 160  
 Val Asn Thr Tyr Tyr Asp Arg Asp Gly Trp Asn Glu Thr Ala Phe Leu  
 165 170 175  
 Lys Pro Ala Asp Gly Leu Thr Ser Ser Ile Thr Arg Tyr Gln Ser Gln  
 180 185 190  
 Pro Glu Val Tyr Ala Thr Pro Arg Asn Leu Leu Trp Ser Tyr Thr Thr  
 195 200 205  
 Arg Thr Thr Val Asn Cys Glu Val Thr Glu Met Ser Ala Arg Ser Met  
 210 215 220  
 Lys Pro Phe Glu Phe Phe Val Thr Ser Val Gly Asp Thr Ile Glu Met  
 225 230 235 240  
 Ser Pro Phe Leu Lys Glu Asn Gly Thr Glu Pro Glu Lys Ile Leu Lys  
 245 250 255  
 Arg Pro His Ser Ile Gln Leu Leu Lys Asn Tyr Ala Val Thr Lys Tyr  
 260 265 270  
 Gly Val Gly Leu Gly Gln Ala Asp Asn Ala Thr Arg Phe Phe Ala Ile  
 275 280 285  
 Phe Gly Asp Tyr Ser Leu Ser Trp Lys Ala Thr Thr Glu Asn Ser Ser  
 290 295 300  
 Tyr Cys Asp Leu Ile Leu Trp Lys Gly Phe Ser Asn Ala Ile Gln Thr  
 305 310 315 320  
 Gln His Asn Ser Ser Leu His Phe Ile Ala Asn Asp Ile Thr Ala Ser  
 325 330 335  
 Phe Ser Thr Pro Leu Glu Glu Ala Asn Phe Asn Glu Thr Phe Lys  
 340 345 350  
 Cys Ile Trp Asn Asn Thr Gln Glu Glu Ile Gln Lys Lys Leu Lys Glu  
 355 360 365  
 Val Glu Lys Thr His Arg Pro Asn Gly Thr Ala Lys Val Tyr Lys Thr  
 370 375 380  
 Thr Gly Asn Leu Tyr Ile Val Trp Gln Pro Leu Ile Gln Ile Asp Leu  
 385 390 395 400

Leu Asp Thr His Ala Lys Leu Tyr Asn Leu Thr Asn Ala Thr Ala Ser  
                   405                  410                  415  
  
 Pro Thr Ser Thr Pro Thr Ser Pro Arg Arg Arg Arg Arg Asp Thr  
                   420                  425                  430  
  
 Ser Ser Val Ser Gly Gly Asn Asn Gly Asp Asn Ser Thr Lys Glu  
                   435                  440                  445  
  
 Glu Ser Val Ala Ala Ser Gln Val Gln Phe Ala Tyr Asp Asn Leu Arg  
                   450                  455                  460  
  
 Lys Ser Ile Asn Arg Val Leu Gly Glu Leu Ser Arg Ala Trp Cys Arg  
                   465                  470                  475                  480  
  
 Glu Gln Tyr Arg Ala Ser Leu Met Trp Tyr Glu Leu Ser Lys Ile Asn  
                   485                  490                  495  
  
 Pro Thr Ser Val Met Ser Ala Ile Tyr Gly Arg Pro Val Ser Ala Lys  
                   500                  505                  510  
  
 Leu Ile Gly Asp Val Val Ser Val Ser Asp Cys Ile Ser Val Asp Gln  
                   515                  520                  525  
  
 Lys Ser Val Phe Val His Lys Asn Met Lys Val Pro Gly Lys Glu Asp  
                   530                  535                  540  
  
 Leu Cys Tyr Thr Arg Pro Val Val Gly Phe Lys Phe Ile Asn Gly Ser  
                   545                  550                  555                  560  
  
 Glu Leu Phe Ala Gly Gln Leu Gly Pro Arg Asn Glu Ile Val Leu Ser  
                   565                  570                  575  
  
 Thr Ser Gln Val Glu Val Cys Gln His Ser Cys Glu His Tyr Phe Gln  
                   580                  585                  590  
  
 Ala Gly Asn Gln Met Tyr Lys Tyr Lys Asp Tyr Tyr Tyr Val Ser Thr  
                   595                  600                  605  
  
 Leu Asn Leu Thr Asp Ile Pro Thr Leu His Thr Met Ile Thr Leu Asn  
                   610                  615                  620  
  
 Leu Ser Leu Val Glu Asn Ile Asp Phe Lys Val Ile Glu Leu Tyr Ser  
                   625                  630                  635                  640  
  
 Lys Thr Glu Lys Arg Leu Ser Asn Val Phe Asp Ile Glu Thr Met Phe  
                   645                  650                  655  
  
 Arg Glu Tyr Asn Tyr Tyr Thr Gln Asn Leu Asn Gly Leu Arg Lys Asp  
                   660                  665                  670  
  
 Leu Asp Asp Ser Ile Asp His Gly Arg Asp Ser Phe Ile Gln Thr Leu  
                   675                  680                  685  
  
 Gly Asp Ile Met Gln Asp Leu Gly Thr Ile Gly Lys Val Val Val Asn  
                   690                  695                  700

Val Ala Ser Gly Val Phe Ser Leu Phe Gly Ser Ile Val Ser Gly Val  
 705 710 715 720  
 Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met Leu Leu Ile Val Leu  
 725 730 735  
 Ile Ile Ala Gly Val Val Val Tyr Leu Phe Met Thr Arg Ser Arg  
 740 745 750  
 Ser Ile Tyr Ser Ala Pro Ile Arg Met Leu Tyr Pro Gly Val Glu Arg  
 755 760 765  
 Ala Ala Gln Glu Pro Gly Ala His Pro Val Ser Glu Asp Gln Ile Arg  
 770 775 780  
 Asn Ile Leu Met Gly Met His Gln Phe Gln Gln Arg Gln Arg Ala Glu  
 785 790 795 800  
 Glu Glu Ala Arg Arg Glu Glu Glu Val Lys Gly Lys Arg Thr Leu Phe  
 805 810 815  
 Glu Val Ile Arg Asp Ser Ala Thr  
 820  
 <210> 44  
 <211> 818  
 <212> PRT  
 <213> Equine herpesvirus 5  
 <400> 44  
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 Leu Ala Leu Leu Cys Gly Arg Val Ala Leu Asp Glu Ser Ser Ala Thr  
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 Pro Ser Ile Pro Pro Thr His Lys Pro Ala Val His His Glu Asp Asn  
 35 40 45  
 Thr Thr Asn Pro Phe Leu Leu Phe Arg Val Cys Gly Ala Ser Pro Thr  
 50 55 60  
 Gly Glu Ile Phe Arg Phe Pro Leu Glu Glu Asn Cys Pro Asn Thr Glu  
 65 70 75 80  
 Asp Lys Glu His Val Glu Gly Ile Leu Leu Ile Tyr Lys Thr Asn Ile  
 85 90 95  
 Val Pro Tyr Ile Phe Asn Val Arg Lys Tyr Arg Lys Leu Val Thr Ser  
 100 105 110  
 Thr Thr Ile Tyr Lys Gly Trp Ser Gln Asp Ala Ile Thr Asn Gln Tyr  
 115 120 125  
 Thr Ser Ser Phe Ala Met Pro Leu Trp Glu Ala Arg Leu Val Asp Tyr  
 130 135 140

Asn Tyr Glu Cys Tyr Asn Gly Ile Gln Val Thr Glu Asn Gly His Leu  
 145 150 155 160  
 Thr Thr Tyr Val Asp Arg Asp Gly Tyr Asn Glu Ser Val Arg Leu Val  
 165 170 175  
 Pro Ala Asp Gly Leu Thr Ser Ser Ile Arg Arg Tyr His Ser Gln Pro  
 180 185 190  
 Glu Leu Tyr Val Thr Pro Arg Asn Leu Leu Trp Ser Tyr Thr Thr Arg  
 195 200 205  
 Thr Thr Val Asn Cys Glu Val Ile Asp Met Thr Ala Arg Ser His Lys  
 210 215 220  
 Pro Phe Glu Tyr Phe Val Thr Ala Ser Gly Asp Ser Ile Glu Thr Ser  
 225 230 235 240  
 Pro Phe Tyr Thr Asn Ala Ser Arg Arg Val Pro Val Gln Val Leu Tyr  
 245 250 255  
 Asn Tyr Ser Val Thr Asp Tyr Gly Val Gly Leu Gly Ser Gly Glu Asn  
 260 265 270  
 Val Thr Arg Phe Phe Ala Thr Leu Asn Asp Phe Ser Ile Ser Trp Lys  
 275 280 285  
 Ala Ala Thr Glu Asn Ser Ser Tyr Cys Pro Leu Val Leu Trp Lys Gly  
 290 295 300  
 Phe Pro Ser Ala Ile Gln Thr Lys His Glu Lys Ser Tyr His Phe Ile  
 305 310 315 320  
 Ala Asp Ala Val Thr Ala Ser Phe Thr Thr Pro Leu Thr Asp Glu Thr  
 325 330 335  
 Ser Tyr Phe Asn Thr Thr Tyr Gln Cys Ala Trp Gln Asp Ile Glu Gly  
 340 345 350  
 Glu Ile Gln Lys Arg Phe Asp Pro Val Ser Lys Thr His Ala Arg Asn  
 355 360 365  
 Gly Ser Val Gln Ile Tyr Lys Thr Ser Gly Asn Leu Tyr Val Val Trp  
 370 375 380  
 Gln Pro Leu Val Gln Leu Asp Leu Leu Ala Ala His Ala Lys Thr Ile  
 385 390 395 400  
 Asn Ser Thr Asp Asn Ser Thr Ser Pro Thr Thr Ala Pro Asn Thr Thr  
 405 410 415  
 Thr Ser Thr Ser Ser Arg Arg Lys Arg Arg Asp Thr Gly Asn Thr Ala  
 420 425 430  
 Thr Asn Asn Ser Ser Asn Asn Ser Ser Met Glu Glu Asn Leu Ala  
 435 440 445

Thr Ser Gln Val Gln Phe Ala Tyr Asp Gln Leu Arg Lys Ser Ile Asn  
 450 455 460  
 Arg Val Leu Glu Gln Leu Ser Arg Val Trp Cys Gln Asn Gln Tyr Arg  
 465 470 475 480  
 Ala Ser Leu Met Trp Tyr Glu Leu Ser Lys Ile Asn Pro Thr Ser Val  
 485 490 495  
 Met Ser Ala Ile Tyr Gly Arg Pro Val Ser Ala Lys Leu Val Gly Asp  
 500 505 510  
 Val Val Gln Ile Ser Asp Cys Ile Thr Val Asp Gln Glu Ser Val Phe  
 515 520 525  
 Val His Arg Asn Leu Arg Val Pro Gly Ser Lys Asp Leu Cys Tyr Thr  
 530 535 540  
 Arg Pro Val Val Gly Phe Lys Phe Ile Asn Gly Ser Glu Leu Phe Val  
 545 550 555 560  
 Gly Gln Leu Gly Ala Arg Asn Glu Ile Leu Leu Ser Thr Asn Leu Val  
 565 570 575  
 Glu Val Cys Gln His Ser Cys Glu His Tyr Phe Gln Gly Gly Asn His  
 580 585 590  
 Ile Tyr Lys Tyr Lys Asn Tyr Glu Tyr Val Ser Thr Met Asn Leu Thr  
 595 600 605  
 Asp Val Pro Thr Leu His Thr Met Ile Thr Leu Asn Leu Ser Leu Val  
 610 615 620  
 Glu Asn Val Asp Phe Gln Val Ile Gln Leu Tyr Ser Gln Lys Glu Lys  
 625 630 635 640  
 Lys Leu Ser Asn Val Phe Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn  
 645 650 655  
 Tyr Tyr Thr Gln Asn Leu Lys Gly Leu Arg Lys Asp Leu Asp Asp Ser  
 660 665 670  
 Ile His Asp Gly Arg Asp Ser Phe Ile Gln Phe Leu Gly Asp Leu Val  
 675 680 685  
 Gln Asp Leu Val Pro Val Gly Asp Val Ile Val Asn Val Ala Ser Gly  
 690 695 700  
 Val Phe Ser Leu Phe Gly Ser Ile Val Ser Gly Val Ile Ser Phe Leu  
 705 710 715 720  
 Lys Asn Pro Leu Gly Ala Ile Leu Thr Ile Ala Leu Ile Val Gly Gly  
 725 730 735  
 Ile Ile Val Leu Tyr Leu Phe Ile Thr Arg Ser Arg Thr Val Tyr Gln  
 740 745 750

Ala Pro Ile Arg Met Leu Tyr Pro Glu Val Asp Arg Ala Pro Gln Gln  
755 760 765

Asn Val Gln Pro Ile Pro Glu Asp Gln Val Arg Ser Ile Leu Leu Ala  
770 775 780

Met His Gln Phe Gln  
785 790 795 800

Glu Glu His Thr Gln Arg Arg Ser Ile Phe Asp Thr Ile Arg Glu Ser  
805 810 815

Thr Ser

<210> 45

<211> 830

<212> PRT

<213> Alcelaphine herpesvirus

<400> 45

Met Ala His Thr Gly Ser Thr Val Cys Ala Phe Leu Ile Phe Ala Val  
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Leu Lys Asn Val Phe Cys Gln Thr Pro Thr Ser Ser Ser Glu Val Glu  
20 25 30

Asp Val Ile Pro Glu Ala Asn Thr Val Ser Asp Asn Ile Ile Arg Gln  
35 40 45

Gln Arg Asn Asn Thr Ala Lys Gly Ile His Ser Asp Pro Ser Ala Phe  
50 55 60

Pro Phe Arg Val Cys Ser Ala Ser Asn Ile Gly Asp Ile Phe Arg Phe  
65 70 75 80

Gln Thr Ser His Ser Cys Pro Asn Thr Lys Asp Lys Glu His Asn Glu  
85 90 95

Gly Ile Leu Leu Ile Phe Lys Glu Asn Ile Val Pro Tyr Val Phe Lys  
100 105 110

Val Arg Lys Tyr Arg Lys Ile Val Thr Thr Ser Thr Ile Tyr Asn Gly  
115 120 125

Ile Tyr Ala Asp Ala Val Thr Asn Gln His Val Phe Ser Lys Ser Val  
130 135 140

Pro Ile Tyr Glu Thr Arg Arg Met Asp Thr Ile Tyr Gln Cys Tyr Asn  
145 150 155 160

Ser Leu Asp Val Thr Val Gly Gly Asn Leu Leu Val Tyr Thr Asp Asn  
165 170 175

Asp Gly Ser Asn Met Thr Val Asp Leu Gln Pro Val Asp Gly Leu Ser  
180 185 190

Asn Ser Val Arg Arg Tyr His Ser Gln Pro Glu Ile His Ala Glu Pro  
 195 200 205  
 Gly Trp Leu Leu Gly Gly Tyr Arg Arg Arg Thr Thr Val Asn Cys Glu  
 210 215 220  
 Val Thr Glu Thr Asp Ala Arg Ala Val Pro Pro Phe Arg Tyr Phe Ile  
 225 230 235 240  
 Thr Asn Ile Gly Asp Thr Ile Glu Met Ser Pro Phe Trp Ser Lys Ala  
 245 250 255  
 Trp Asn Glu Thr Glu Phe Ser Gly Glu Pro Asp Arg Thr Leu Thr Val  
 260 265 270  
 Ala Lys Asp Tyr Arg Val Val Asp Tyr Lys Phe Arg Gly Thr Gln Pro  
 275 280 285  
 Gln Gly His Thr Arg Ile Phe Val Asp Lys Glu Glu Tyr Thr Leu Ser  
 290 295 300  
 Trp Ala Gln Gln Phe Arg Asn Ile Ser Tyr Cys Arg Trp Ala His Trp  
 305 310 315 320  
 Lys Ser Phe Asp Asn Ala Ile Lys Thr Glu His Gly Lys Ser Leu His  
 325 330 335  
 Phe Val Ala Asn Asp Ile Thr Ala Ser Phe Tyr Thr Pro Asn Thr Gln  
 340 345 350  
 Thr Arg Glu Val Leu Gly Lys His Val Cys Leu Asn Asn Thr Ile Glu  
 355 360 365  
 Ser Glu Leu Lys Ser Arg Leu Ala Lys Val Asn Asp Thr His Ser Pro  
 370 375 380  
 Asn Gly Thr Ala Gln Tyr Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val  
 385 390 395 400  
 Trp Gln Pro Leu Val Gln Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu  
 405 410 415  
 Asp Ala Val Lys Lys Gln Gln Asn Thr Thr Thr Thr Thr Thr Thr  
 420 425 430  
 Arg Ser Arg Arg Gln Arg Arg Ser Val Ser Ser Gly Ile Asp Asp Val  
 435 440 445  
 Tyr Thr Ala Glu Ser Thr Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr  
 450 455 460  
 Asp Thr Leu Arg Ala Gln Ile Asn Asn Val Leu Glu Glu Leu Ser Arg  
 465 470 475 480  
 Ala Trp Cys Arg Glu Gln His Arg Ala Ser Leu Met Trp Asn Glu Leu  
 485 490 495

Ser Lys Ile Asn Pro Thr Ser Val Met Ser Ser Ile Tyr Gly Arg Pro  
 500 505 510  
 Val Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser His Cys Val  
 515 520 525  
 Val Val Asp Gln Asp Ser Val Ser Leu His Arg Ser Met Arg Val Pro  
 530 535 540  
 Gly Arg Asp Lys Thr His Glu Cys Tyr Ser Arg Pro Pro Val Thr Phe  
 545 550 555 560  
 Lys Phe Ile Asn Asp Ser His Leu Tyr Lys Gly Gln Leu Gly Val Asn  
 565 570 575  
 Asn Glu Ile Leu Leu Thr Thr Ala Val Glu Ile Cys His Glu Asn  
 580 585 590  
 Thr Glu His Tyr Phe Gln Gly Gly Asn Asn Met Tyr Phe Tyr Lys Asn  
 595 600 605  
 Tyr Arg His Val Lys Thr Met Pro Val Gly Asp Val Ala Thr Leu Asp  
 610 615 620  
 Thr Phe Met Val Leu Asn Leu Thr Leu Val Glu Asn Ile Asp Phe Gln  
 625 630 635 640  
 Val Ile Glu Leu Tyr Ser Arg Glu Glu Lys Arg Met Ser Thr Ala Phe  
 645 650 655  
 Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Val  
 660 665 670  
 Thr Gly Leu Arg Arg Asp Leu Thr Asp Leu Ala Thr Asn Arg Asn Gln  
 675 680 685  
 Phe Val Asp Ala Phe Gly Ser Leu Met Asp Asp Leu Gly Val Val Gly  
 690 695 700  
 Lys Thr Val Leu Asn Ala Val Ser Ser Val Ala Thr Leu Phe Ser Ser  
 705 710 715 720  
 Ile Val Ser Gly Ile Ile Asn Phe Ile Lys Asn Pro Phe Gly Gly Met  
 725 730 735  
 Leu Leu Phe Gly Leu Ile Ala Ala Val Val Ile Thr Val Ile Leu Leu  
 740 745 750  
 Asn Arg Lys Ala Lys Arg Phe Ala Gln Asn Pro Val Gln Met Ile Tyr  
 755 760 765  
 Pro Asp Ile Lys Thr Ile Thr Ser Gln Arg Glu Glu Leu Gln Val Asp  
 770 775 780  
 Pro Ile Ser Lys His Glu Leu Asp Arg Ile Met Leu Ala Met His Asp  
 785 790 795 800

Tyr His Ala Ser Lys Gln Pro Glu Ser Lys Gln Asp Glu Glu Gln Gly  
                   805                  810                  815  
 Ser Thr Thr Ser Gly Pro Ala Asp Trp Leu Asn Lys Ala Lys  
                   820                  825                  830  
 <210> 46  
 <211> 829  
 <212> PRT  
 <213> Epstein-Barr virus  
 <400> 46  
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 Ala Cys Arg Leu Gly Ala Gln Thr Pro Glu Gln Pro Ala Pro Pro Ala  
   20            25                  30  
 Thr Thr Val Gln Pro Thr Ala Thr Arg Gln Gln Thr Ser Phe Pro Phe  
   35            40                  45  
 Arg Val Cys Glu Leu Ser Ser His Gly Asp Leu Phe Arg Phe Ser Ser  
   50            55                  60  
 Asp Ile Gln Cys Pro Ser Phe Gly Thr Arg Glu Asn His Thr Glu Gly  
   65            70                  75                  80  
 Leu Leu Met Val Phe Lys Asp Asn Ile Ile Pro Tyr Ser Phe Lys Val  
   85            90                  95  
 Arg Ser Tyr Thr Lys Ile Val Thr Asn Ile Leu Ile Tyr Asn Gly Trp  
  100           105                  110  
 Tyr Ala Asp Ser Val Thr Asn Arg His Glu Glu Lys Phe Ser Val Asp  
  115           120                  125  
 Ser Tyr Glu Thr Asp Gln Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ala  
  130           135                  140  
 Val Lys Met Thr Lys Asp Gly Leu Thr Arg Val Tyr Val Asp Arg Asp  
  145           150                  155                  160  
 Gly Val Asn Ile Thr Val Asn Leu Lys Pro Thr Gly Gly Leu Ala Asn  
  165           170                  175  
 Gly Val Arg Arg Tyr Ala Ser Gln Thr Glu Leu Tyr Asp Ala Pro Gly  
  180           185                  190  
 Trp Leu Ile Trp Thr Tyr Arg Thr Arg Thr Val Asn Cys Leu Ile  
  195           200                  205  
 Thr Asp Met Met Ala Lys Ser Asn Ser Pro Phe Asp Phe Phe Val Thr  
  210           215                  220  
 Thr Thr Gly Gln Thr Val Glu Met Ser Pro Phe Tyr Asp Gly Lys Asn  
  225           230                  235                  240

Lys Glu Thr Phe His Glu Arg Ala Asp Ser Phe His Val Arg Thr Asn  
                   245                  250                  255  
 Tyr Lys Ile Val Asp Tyr Asp Asn Arg Gly Thr Asn Pro Gln Gly Glu  
                   260                  265                  270  
 Arg Arg Ala Phe Leu Asp Lys Gly Thr Tyr Thr Leu Ser Trp Lys Leu  
                   275                  280                  285  
 Glu Asn Arg Thr Ala Tyr Cys Pro Leu Gln His Trp Gln Thr Phe Asp  
                   290                  295                  300  
 Ser Thr Ile Ala Thr Glu Thr Gly Lys Ser Ile His Phe Val Thr Asp  
                   305                  310                  315                  320  
 Glu Gly Thr Ser Ser Phe Val Thr Asn Thr Thr Val Gly Ile Glu Leu  
                   325                  330                  335  
 Pro Asp Ala Phe Lys Cys Ile Glu Glu Gln Val Asn Lys Thr Met His  
                   340                  345                  350  
 Glu Lys Tyr Glu Ala Val Gln Asp Arg Tyr Thr Lys Gly Gln Glu Ala  
                   355                  360                  365  
 Ile Thr Tyr Phe Ile Thr Ser Gly Gly Leu Leu Leu Ala Trp Leu Pro  
                   370                  375                  380  
 Leu Thr Pro Arg Ser Leu Ala Thr Val Lys Asn Leu Thr Glu Leu Thr  
                   385                  390                  395                  400  
 Thr Pro Thr Ser Ser Pro Pro Ser Ser Pro Ser Pro Ala Pro Ser  
                   405                  410                  415  
 Ala Ala Arg Gly Ser Thr Pro Ala Ala Val Leu Arg Arg Arg Arg Arg  
                   420                  425                  430  
 Asp Ala Gly Asn Ala Thr Thr Pro Val Pro Pro Thr Ala Pro Gly Lys  
                   435                  440                  445  
 Ser Leu Gly Thr Leu Asn Asn Pro Ala Thr Val Gln Ile Gln Phe Ala  
                   450                  455                  460  
 Tyr Asp Ser Leu Arg Arg Gln Ile Asn Arg Met Leu Gly Asp Leu Ala  
                   465                  470                  475                  480  
 Arg Ala Trp Cys Leu Glu Gln Lys Arg Gln Asn Met Val Leu Arg Glu  
                   485                  490                  495  
 Leu Thr Lys Ile Asn Pro Thr Thr Val Met Ser Ser Ile Tyr Gly Lys  
                   500                  505                  510  
 Ala Val Ala Ala Lys Arg Leu Gly Asp Val Ile Ser Val Ser Gln Cys  
                   515                  520                  525  
 Val Pro Val Asn Gln Ala Thr Val Thr Leu Arg Lys Ser Met Arg Val  
                   530                  535                  540

Pro Gly Ser Glu Thr Met Cys Tyr Ser Arg Pro Leu Val Ser Phe Ser  
 545 550 555 560  
 Phe Ile Asn Asp Thr Lys Thr Tyr Glu Gly Gln Leu Gly Thr Asp Asn  
 565 570 575  
 Glu Ile Phe Leu Thr Lys Lys Met Thr Glu Val Cys Gln Ala Thr Ser  
 580 585 590  
 Gln Tyr Tyr Phe Gln Ser Gly Asn Glu Ile His Val Tyr Asn Asp Tyr  
 595 600 605  
 His His Phe Lys Thr Ile Glu Leu Asp Gly Ile Ala Thr Leu Gln Thr  
 610 615 620  
 Phe Ile Ser Leu Asn Thr Ser Leu Ile Glu Asn Ile Asp Phe Ala Ser  
 625 630 635 640  
 Leu Glu Leu Tyr Ser Arg Asp Glu Gln Arg Ala Ser Asn Val Phe Asp  
 645 650 655  
 Leu Glu Gly Ile Phe Arg Glu Tyr Asn Phe Gln Ala Gln Asn Ile Ala  
 660 665 670  
 Gly Leu Arg Lys Asp Leu Asp Asn Ala Val Ser Asn Gly Arg Asn Gln  
 675 680 685  
 Phe Val Asp Gly Leu Gly Glu Leu Met Asp Ser Leu Gly Ser Val Gly  
 690 695 700  
 Gln Ser Ile Thr Asn Leu Val Ser Thr Val Gly Gly Leu Phe Ser Ser  
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 Leu Val Ser Gly Phe Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met  
 725 730 735  
 Leu Ile Leu Val Leu Val Ala Gly Val Val Ile Leu Val Ile Ser Leu  
 740 745 750  
 Thr Arg Arg Thr Arg Gln Met Ser Gln Gln Pro Val Gln Met Leu Tyr  
 755 760 765  
 Pro Gly Ile Asp Glu Leu Ala Gln Gln His Ala Ser Gly Glu Gly Pro  
 770 775 780  
 Gly Ile Asn Pro Ile Ser Lys Thr Glu Leu Gln Ala Ile Met Leu Ala  
 785 790 795 800  
 Leu His Glu Gln Asn Gln Glu Gln Lys Arg Ala Ala Gln Arg Ala Ala  
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 Gly Pro Ser Val Ala Ser Arg Ala Leu Gln Ala Ala Arg  
 820 825  
 <210> 47  
 <211> 660  
 <212> DNA

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 641-1300

<400> 47

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cgcaggggcg	caacttcacg	gagggatcg	ccgtgcttt	caaggagaac	atcgccccgc	120
acaagtcaa	ggcccacatc	tactacaaga	acgtcatcg	cacgaccgtg	tggtccggaa	180
gcacgtacgc	ggccatcacg	aaccgcttca	cagaccgcgt	gcccgcccc	gtgcaggaga	240
tcacggacgt	gatcgaccgc	cgcggcaagt	gcgtctccaa	ggccgagta	gtgcgcaaca	300
accacaaggt	gaccgccttc	gaccgcgacg	agaaccccgt	cgaggtggac	ctgcgcccct	360
cgccgctgaa	cgcgctcgcc	acccgcggct	ggcacaccac	caacgacacc	tacaccaaga	420
tcggcgccgc	gggcttctac	cacacgggca	cctccgtcaa	ctgcatcg	gaggaggtgg	480
aggcgcgctc	cgtgtacccc	tacgactct	tcgcccgtc	cacggggac	attgtgtaca	540
tgtccccctt	atacggccctg	cgcgaggggg	cccacgggaa	gcacatcg	tacgcgcccgg	600
ggcgcttcca	gcaggtggag	cactactacc	ccatcgac	ggactcg	ctccgcgcct	660

<210> 48

<211> 359

<212> PRT

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 491-850

<400> 48

Ala	Ala	Pro	Ala	Ala	Ala	Arg	Arg	Ala	Arg	Arg	Ser	Pro	Gly	Pro	Ala
1			5				10					15			

Gly	Thr	Pro	Glu	Pro	Pro	Ala	Val	Asn	Gly	Thr	Gly	His	Leu	Arg	Ile
						20		25				30			

Thr	Thr	Gly	Ser	Ala	Glu	Phe	Ala	Arg	Leu	Gln	Phe	Thr	Tyr	Asp	His
				35			40				45				

Ile	Gln	Ala	His	Val	Asn	Asp	Met	Leu	Gly	Arg	Ile	Ala	Ala	Ala	Trp
				50		55			60						

Cys	Glu	Leu	Gln	Asn	Lys	Asp	Arg	Thr	Leu	Trp	Ser	Glu	Met	Ser	Arg
65					70			75			80				

Leu	Asn	Pro	Ser	Ala	Val	Ala	Thr	Ala	Ala	Leu	Gly	Gln	Arg	Val	Ser
					85			90			95				

Ala	Arg	Met	Leu	Gly	Asp	Val	Met	Ala	Ile	Ser	Arg	Cys	Val	Glu	Val
			100				105				110				

Arg	Gly	Gly	Val	Tyr	Val	Gln	Asn	Ser	Met	Arg	Val	Pro	Gly	Glu	Arg
			115			120			125						

Gly	Thr	Cys	Tyr	Ser	Arg	Pro	Leu	Val	Thr	Phe	Glu	His	Asn	Gly	Thr
					130			135			140				

Gly	Val	Ile	Glu	Gly	Gln	Leu	Gly	Asp	Asp	Asn	Glu	Leu	Leu	Ile	Ser
145					150				155		160				

Arg Asp Leu Ile Glu Pro Cys Thr Gly Asn His Arg Arg Tyr Phe Lys  
 165 170 175  
 Leu Gly Ser Gly Tyr Val Tyr Tyr Glu Asp Tyr Asn Tyr Val Arg Met  
 180 185 190  
 Val Glu Val Pro Glu Thr Ile Ser Thr Arg Val Thr Leu Asn Leu Thr  
 195 200 205  
 Leu Leu Glu Asp Arg Glu Phe Leu Pro Leu Glu Val Tyr Thr Arg Glu  
 210 215 220  
 Glu Leu Ala Asp Thr Gly Leu Leu Asp Tyr Ser Glu Ile Gln Arg Arg  
 225 230 235 240  
 Asn Gln Leu His Ala Leu Lys Phe Tyr Asp Ile Asp Arg Val Val Lys  
 245 250 255  
 Val Asp His Asn Val Val Leu Leu Arg Gly Ile Ala Asn Phe Phe Gln  
 260 265 270  
 Gly Leu Gly Asp Val Gly Ala Ala Val Gly Lys Val Val Leu Gly Ala  
 275 280 285  
 Thr Gly Ala Val Ile Ser Ala Val Gly Gly Met Val Ser Phe Leu Ser  
 290 295 300  
 Asn Pro Phe Gly Ala Leu Ala Ile Gly Leu Leu Val Leu Ala Gly Leu  
 305 310 315 320  
 Val Ala Ala Phe Leu Ala Tyr Arg His Ile Ser Arg Leu Arg Arg Asn  
 325 330 335  
 Pro Met Lys Ala Leu Tyr Pro Val Thr Thr Lys Thr Leu Lys Glu Asp  
 340 345 350  
 Gly Val Asp Glu Gly Asp Val  
 355  
 <210> 49  
 <211> 420  
 <212> DNA  
 <213> Suid herpesvirus 2  
 <400> 49  
 ccagcataat gatagccaat aatctgtgtt actctaccct gatcttaaat gacgaggacg 60  
 tgacggggat cgacgagaaa gatattctga cggtgcatgt aaacaagaat accgtgtaca 120  
 ggttcgtag gggcgcgtc agggagtcta tactcggcac gctgctgtct agatggctca 180  
 ggaagagaaa ggaagtgaag ggcgcgtca aacgctgtga ggaccctatg ttggcactga 240  
 tacttgacaa gcagcagctt gcccctaagg tgacgtgcaa tgcgtttac ggcttcacgg 300  
 gagccgtgca cggctctgctg ccgtgtctcc ctctagcggc gtccatcacc agcataggc 360  
 gggacatgct taggcagacg agtacttta tcaacaatgt ccttcgtct agagaatacg 420  
 <210> 50  
 <211> 159

<212> PRT  
 <213> Suid herpesvirus 2

<400>	50		
Ser Ile Met Ile Ala Asn Asn Leu Cys Tyr Ser Thr Leu Ile Leu Asn			
1	5	10	15
Asp Glu Asp Val Thr Gly Ile Asp Glu Lys Asp Ile Leu Thr Val His			
20	25	30	
Val Asn Lys Asn Thr Val Tyr Arg Phe Val Arg Ser Ser Val Arg Glu			
35	40	45	
Ser Ile Leu Gly Thr Leu Leu Ser Arg Trp Leu Arg Lys Arg Lys Glu			
50	55	60	
Val Lys Ala Arg Met Lys Arg Cys Glu Asp Pro Met Leu Ala Leu Ile			
65	70	75	80
Leu Asp Lys Gln Gln Leu Ala Leu Lys Val Thr Cys Asn Ala Phe Tyr			
85	90	95	
Gly Phe Thr Gly Ala Val His Gly Leu Leu Pro Cys Leu Pro Leu Ala			
100	105	110	
Ala Ser Ile Thr Ser Ile Gly Arg Asp Met Leu Arg Gln Thr Ser Asp			
115	120	125	
Phe Ile Asn Asn Val Leu Ser Ser Arg Glu Tyr Val Ser Glu Lys Phe			
130	135	140	
Ser Leu Ser Asp Gly Asp Phe Gln Gly Asp Phe Ser Pro Glu Cys			
145	150	155	

<210> 51  
 <211> 466  
 <212> DNA  
 <213> artificial

<220>  
 <223> Portion of porcine gamma herpesvirus polymerase - AF118399

<400>	51
taatctatgt cactctaccc taatccatca tgaagacctg cataaaatatc ctcaattaaa	60
ggaggaggat tatgaaacat ttttGattAG ttctggtcct gttcactttg taaaaaaaca	120
cataatcagaa tctcttctgt ctaacctgct tacaacatgg ctggctaaga gaaaaatgat	180
cagaaaaggaa ttagcagcat gtgctgaccc aaagctcagg acaattttag ataaacagca	240
gcttgcaatt aaggtgacat gcaatgtgt gtatgggttc actggtgttgcatctggat	300
gctgccctgt ctcaagattg cagagaccat aactatgca ggaaggccat tgttggaaaa	360
gacaaaagta tttgttagaga atttaagtca tgaggatctc cattccatct gtaagggtgg	420
ctttatgcct cagtcaccaa acagcattga taaacccttc aagggt	466

<210> 52  
 <211> 423  
 <212> DNA  
 <213> artificial

<220>

<223> Portion of porcine gamma herpesvirus polymerase - AF118401

<400> 52

gaggacctgc	ataagtatcc	tcaattaaag	gaggatgatt	atgaaacatt	tttgattagt	60
tctggccctg	ttcacttgt	aaaaaaacac	atatcagaat	ctctctgtc	gaacttgc	120
acaacatggc	tggccaagag	aaaaatgatc	agaaaggaat	tgacagcatg	tgctgatcca	180
aagctcagga	caatttaga	taaacacgcag	cttgcaatta	aggtgacatg	caatgctgtg	240
tatggattca	ctggtgttc	atctggatg	ctgccatgtc	tcaagattgc	agagaccatc	300
actatgcaag	gaagggccat	gttggaaaag	acaaaagtat	tttagagaaa	tctgagtc	360
gaagatctcc	gttccatatg	taaggttgc	tctatacctc	agtcatcaaa	cgtgtttgat	420
aaa						423

<210> 53

<211> 292

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 53

aagtaataga	actatactct	agagaagaga	agaggatgag	cactgcattt	gatatacgaga	60
ccatgtttag	agaatacaac	tactacacac	agagggtcac	tggcctgcgg	aggacttga	120
cagacctagc	tacaaacaga	aatcaatttg	tagatgcctt	tggcagcctc	atggacgact	180
tgggggtcgt	ggggaaaacg	gtgttgaatg	ctgtgagcag	tgtggccaca	ctcttcagct	240
ctatagtctc	agggatcatc	aatttcatta	aaaacccctt	tggggaaatg	tt	292

<210> 54

<211> 152

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 54

tgggccgtg	agcagcacccg	agcctctctc	atgtggaaacg	agctaagcaa	aatcaaccct	60
accagtgtga	tgagctctat	atacgggggg	ccagtatctg	ccaaaagaat	tggagatgt	120
atatctgtct	ctcactgtgt	ggtgtggac	ca			152

<210> 55

<211> 793

<212> PRT

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 55

Lys	Gly	Ile	His	Ser	Asp	Pro	Ser	Ala	Phe	Pro	Phe	Arg	Val	Cys	Ser
1				5				10					15		

Ala Ser Asn Ile Gly Asp Ile Phe Arg Phe Gln Thr Ser His Ser Cys  
 20 25 30

Pro Asn Thr Lys Asp Lys Glu His Asn Glu Gly Ile Leu Leu Ile Phe  
 35 40 45

Lys Glu Asn Ile Val Pro Tyr Val Phe Lys Val Arg Lys Tyr Arg Lys  
 50 55 60

Ile Val Thr Thr Ser Thr Ile Tyr Asn Gly Ile Tyr Ala Asp Ala Val  
 65 70 75 80

Thr Asn Gln His Val Phe Ser Lys Ser Val Pro Ile Tyr Glu Thr Arg  
 85 90 95

Arg Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ser Leu Asp Val Thr Val  
 100 105 110

Gly Gly Asn Leu Leu Val Tyr Thr Asp Asn Asp Gly Ser Asn Met Thr  
 115 120 125

Val Asp Leu Gln Pro Val Asp Gly Leu Ser Asn Ser Val Arg Arg Tyr  
 130 135 140

His Ser Gln Pro Glu Ile His Ala Glu Pro Gly Trp Leu Leu Gly Gly  
 145 150 155 160

Tyr Arg Arg Arg Thr Thr Val Asn Cys Glu Val Thr Glu Thr Asp Ala  
 165 170 175

Arg Ala Val Pro Pro Phe Arg Tyr Phe Ile Thr Asn Ile Gly Asp Thr  
 180 185 190

Ile Glu Met Ser Pro Phe Trp Ser Lys Ala Trp Asn Glu Thr Glu Phe  
 195 200 205

Ser Gly Glu Pro Asp Arg Thr Leu Thr Val Ala Lys Asp Tyr Arg Val  
 210 215 220

Val Asp Tyr Lys Phe Arg Gly Thr Gln Pro Gln Gly His Thr Arg Ile  
 225 230 235 240

Phe Val Asp Lys Glu Glu Tyr Thr Leu Ser Trp Ala Gln Gln Phe Arg  
 245 250 255

Asn Ile Ser Tyr Cys Arg Trp Ala His Trp Lys Ser Phe Asp Asn Ala  
 260 265 270

Ile Lys Thr Glu His Gly Lys Ser Leu His Phe Val Ala Asn Asp Ile  
 275 280 285

Thr Ala Ser Phe Tyr Thr Pro Asn Thr Gln Thr Arg Glu Val Leu Gly  
 290 295 300

Lys His Val Cys Leu Asn Asn Thr Ile Glu Ser Glu Leu Lys Ser Arg  
 305 310 315 320

Leu Ala Lys Val Asn Asp Thr His Ser Pro Asn Gly Thr Ala Gln Tyr  
                  325                     330                 335  
  
 Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val Trp Gln Pro Leu Val Gln  
                  340                     345                 350  
  
 Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu Asp Ala Val Lys Lys Gln  
                  355                     360                 365  
  
 Gln Asn Thr Thr Thr Thr Thr Arg Ser Arg Arg Gln Arg  
                  370                     375                 380  
  
 Arg Ser Val Ser Ser Gly Ile Asp Asp Val Tyr Thr Ala Glu Ser Thr  
                  385                     390                 395                 400  
  
 Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr Asp Thr Leu Arg Ala Gln  
                  405                     410                 415  
  
 Ile Asn Asn Val Leu Glu Glu Leu Ser Arg Ala Trp Cys Arg Glu Gln  
                  420                     425                 430  
  
 His Arg Ala Ser Leu Met Trp Asn Glu Leu Ser Lys Ile Asn Pro Thr  
                  435                     440                 445  
  
 Ser Val Met Ser Ser Ile Tyr Gly Arg Pro Val Ser Ala Lys Arg Ile  
                  450                     455                 460  
  
 Gly Asp Val Ile Ser Val Ser His Cys Val Val Val Asp Gln Asp Ser  
                  465                     470                 475                 480  
  
 Val Ser Leu His Arg Ser Met Arg Val Pro Gly Arg Asp Lys Thr His  
                  485                     490                 495  
  
 Glu Cys Tyr Ser Arg Pro Pro Val Thr Phe Lys Phe Ile Asn Asp Ser  
                  500                     505                 510  
  
 His Leu Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu Ile Leu Leu Thr  
                  515                     520                 525  
  
 Thr Thr Ala Val Glu Ile Cys His Glu Asn Thr Glu His Tyr Phe Gln  
                  530                     535                 540  
  
 Gly Gly Asn Asn Met Tyr Phe Tyr Lys Asn Tyr Arg His Val Lys Thr  
                  545                     550                 555                 560  
  
 Met Pro Val Gly Asp Val Ala Thr Leu Asp Thr Phe Met Val Leu Asn  
                  565                     570                 575  
  
 Leu Thr Leu Val Glu Asn Ile Asp Phe Gln Val Ile Glu Leu Tyr Ser  
                  580                     585                 590  
  
 Arg Glu Glu Lys Arg Met Ser Thr Ala Phe Asp Ile Glu Thr Met Phe  
                  595                     600                 605  
  
 Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Val Thr Gly Leu Arg Arg Asp  
                  610                     615                 620

Leu Thr Asp Leu Ala Thr Asn Arg Asn Gln Phe Val Asp Ala Phe Gly  
625 630 635 640

Ser Leu Met Asp Asp Leu Gly Val Val Gly Lys Thr Val Leu Asn Ala  
645 650 655

Val Ser Ser Val Ala Thr Leu Phe Ser Ser Ile Val Ser Gly Ile Ile  
660 665 670

Asn Phe Ile Lys Asn Pro Phe Gly Gly Met Leu Leu Phe Gly Leu Ile  
675 680 685

Ala Ala Val Val Ile Thr Val Ile Leu Leu Asn Arg Lys Ala Lys Arg  
690 695 700

Phe Ala Gln Asn Pro Val Gln Met Ile Pro Asp Ile Lys Thr Ile Thr  
705 710 715 720

Ser Gln Arg Glu Glu Leu Gln Val Asp Pro Ile Ser Lys His Glu Leu  
725 730 735

Asp Arg Ile Met Leu Ala Met His Asp Tyr His Ala Ser Lys Gln Pro  
740 745 750

Glu Ser Lys Gln Asp Glu Glu Gln Gly Ser Thr Thr Ser Gly Pro Ala  
755 760 765

Asp Leu Asn Lys Ala Lys Asn Val Leu Arg Arg Arg Ala Gly Tyr Lys  
770 775 780

Pro Leu Lys Arg Thr Asp Ser Phe Glu  
785 790